

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 16:15:41 ; Search time 184 Seconds
(without alignments)
21.491 Million cell updates/sec

Title: US-09-684-361C-144
Perfect score: 52
Sequence: 1 NAPYLPSC L 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	9	3 AAY98629	Aay98629 Wtl deriv
2	52	100.0	9	3 AAY98767	Aay98767 Wtl deriv
3	52	100.0	9	4 AAG62099	Aag62099 Mouse Wtl
4	52	100.0	9	4 AAG61961	Aag61961 Human Wtl
5	52	100.0	9	4 AAU68866	Aau68866 Mouse Wtl
6	52	100.0	9	4 AAU68728	Aau68728 Human Wtl
7	52	100.0	9	5 ABG33336	Abg33336 Mouse Wtl
8	52	100.0	9	5 ABG33198	Abg33198 Human Wtl
9	52	100.0	9	7 ADB67484	Adb67484 Mouse Wtl
10	52	100.0	9	7 ADB67346	Adb67346 Human Wtl
11	52	100.0	9	7 ADJ80579	Adj80579 Wilm's tu
12	52	100.0	9	8 ADJ80717	Adj80717 Wilm's tu
13	52	100.0	9	8 ADJ83637	Adj83637 Murine Wtl
14	52	100.0	9	8 ADJ83499	Adj83499 Human Wtl
15	52	100.0	9	8 ADL57525	Adl57525 Mouse Wtl
16	52	100.0	9	8 ADL57387	Adl57387 Human Wtl
17	52	100.0	9	8 ADO09080	Ado09080 Mouse Wtl
18	52	100.0	9	8 ADO08942	Ado08942 Human Wtl
19	52	100.0	9	8 ADQ79604	Adq79604 Human Wtl
20	52	100.0	23	3 AAY98502	Aay98502 Human Wtl
21	52	100.0	23	3 AAY98503	Aay98503 Mouse Wtl
22	52	100.0	23	4 AAG61834	Aag61834 Human Wtl
23	52	100.0	23	4 AAG61835	Aag61835 Mouse Wtl
24	52	100.0	23	4 AAU68601	Aau68601 Human Wtl

25	52	100.0	23	4 AAU68602	Aau68602 Mouse Wtl
26	52	100.0	23	5 ABG33072	Abg33072 Mouse Wtl
27	52	100.0	23	5 ABG33071	Abg33071 Human Wtl
28	52	100.0	23	7 ADB67204	Adb67204 Human/mou
29	52	100.0	23	7 ADB67205	Adb67205 Human/mou
30	52	100.0	23	7 ADJ80437	Adj80437 Wilm's tu
31	52	100.0	23	7 ADJ80438	Adj80438 Wilm's tu
32	52	100.0	23	8 ADJ83357	Adj83357 Human Wtl
33	52	100.0	23	8 ADJ83358	Adj83358 Murine Wtl
34	52	100.0	23	8 ADL57246	Adl57246 Mouse Wtl
35	52	100.0	23	8 ADL57245	Adl57245 Human Wtl
36	52	100.0	23	8 ADO08800	Ado08800 Human Wtl
37	52	100.0	23	8 ADO08801	Ado08801 Mouse Wtl
38	52	100.0	152	5 ABG33387	Abg33387 Human Wtl
39	52	100.0	152	7 ADB67545	Adb67545 Human pro
40	52	100.0	152	7 ADJ80778	Adj80778 Wilm's tu
41	52	100.0	152	8 ADJ83698	Adj83698 Human Wtl
42	52	100.0	152	8 ADL57586	Adl57586 Human Wtl
43	52	100.0	152	8 ADO09141	Ado09141 Human Wtl
44	52	100.0	154	2 AAU47175	Aau47175 Wilm's tu
45	52	100.0	154	5 AAG78445	Aag78445 Amino aci

ALIGNMENTS

RESULT 1
AAY98629
ID AAY98629 standard; peptide; 9 AA.
XX AC AAY98629;
XX DT 31-JUL-2000 (first entry)
XX DE WT1 derived immunogenic peptide SEQ ID NO:144.
XX KW WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
KW metastatic disease; mouse; human; Wilm's tumour; immune response;
KW vaccine.
XX OS Homo sapiens.
XX PN WO200018795-A2.
XX PD 06-APR-2000.
XX PF 30-SEP-1999; 99WO-US022819.
XX PR 30-SEP-1998; 98US-00164223.
PR 25-MAR-1999; 99US-00276484.
(CORI-) CORIXA CORP.
(GAIG/) GAIGER A.
Gaiger A, Cheever M;
WPI; 2000-293107/25.
Novel polypeptides comprising an immunogenic portion of a native Wtl
polypeptide, useful for inhibiting the development of malignant diseases
associated with Wtl expression e.g. leukemia or cancer.

Claim 4; Page 165; 193pp; English.

The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, Wtl, (or variants of the immunogenic portion retaining the ability to react with Wtl-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native Wtl polypeptide. The polypeptides are useful therapeutically and to manufacture medicaments for enhancing/inducing an immune response in patients. The polypeptides, mimetics or polynucleotides can be included with a carrier/excipient in pharmaceutical compositions or with a non-

CC specific immune response enhancer (e.g. an adjuvant or enhancer
CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
CC compositions and vaccines can be administered to human patients to
CC enhance or induce an immune response specific for Wt1 or a cell
CC expressing Wt1, useful to inhibit the development of malignant diseases
CC associated with Wt1 expression, e.g. leukemia (especially acute/chronic
CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
CC AA13848 to AA13862 represent polypeptide sequences, and AA13848 to
CC present invention
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCL 9
DB 1 NAPYLPSCL 9

RESULT 2
AA13862 standard; peptide; 9 AA.
XX
AC AA13862;
XX
DT 31-JUL-2000 (first entry)
XX
DE Wt1 derived immunogenic peptide SEQ ID NO:282.
XX
KW Wt1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
KW metastatic disease; mouse; human; Wilm's tumour; immune response;
KW vaccine.
XX
OS Mus musculus.
XX
FN WO200018795-A2.
XX
PD 06-APR-2000.
XX
PF 30-SEP-1999; 99WO-US022819.
XX
PR 30-SEP-1998; 98US-00164223.
PR 25-MAR-1999; 99US-00276484.
XX
PA (CORI-) CORIXA CORP.
PA (GAIG/) GAIGER A.
XX
PI Gaiger A, Cheever M;
XX
DR WPI; 2000-293107/25.
XX
XX
XX Novel polypeptides comprising an immunogenic portion of a native Wt1
XX polypeptide, useful for inhibiting the development of malignant diseases
XX associated with Wt1 expression e.g. leukemia or cancer.
XX
XX Claim 4; Page 185; 193pp; English.
XX
XX The present invention describes polypeptides (I) comprising an
XX immunogenic portion of a native Wilm's Tumour gene product polypeptide,
XX Wt1 (or variants of the immunogenic portion retaining the ability to
XX react with Wt1-specific antisera and/or T-cell lines or clones) and
XX comprising 16 consecutive amino acids (aa) or less of a native Wt1
XX polypeptide. The polypeptides are useful therapeutically and to
XX manufacture medicaments for enhancing/inducing an immune response in
XX patients. The polypeptides, mimetics or polynucleotides can be included
XX with carrier/exipient in pharmaceutical compositions or with a non-
XX specific immune response enhancer (e.g. an adjuvant or enhancer
XX preferentially enhancing a T cell response) in vaccines. Pharmaceutical
XX compositions and vaccines can be administered to human patients to

CC enhance or induce an immune response specific for Wt1 or a cell
CC expressing Wt1, useful to inhibit the development of malignant diseases
CC associated with Wt1 expression, e.g. leukemia (especially acute/chronic
CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
CC AA13848 to AA13862 represent polypeptide sequences, and AA13848 to
CC present invention
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCL 9
DB 1 NAPYLPSCL 9

RESULT 3
AAG62099 standard; peptide; 9 AA.
XX
ID AAG62099
XX
AC AAG62099;
XX
DT 06-JUL-2001 (first entry)
XX
DE Mouse Wt1 immunogenic peptide SEQ ID NO: 282.
XX
KW Human; mouse; immunotherapy; cancer; leukaemia; Wt1; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor.
XX
OS Mus musculus.
XX
FN WO200125273-A2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000WO-US027465.
XX
PR 04-OCT-1999; 99US-0157459P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Xu J, Cheever MA, Reed SG;
XX
DR WPI; 2001-328324/34.
XX
XX Polypeptide comprising part of the Wilm's Tumour gene product sequence is
XX used in the diagnosis and treatment of malignant diseases e.g. leukemia
XX and cancer associated with Wt1.
XX
XX Claim 4; Page 198; 228pp; English.
XX
XX The present invention describes compositions comprising peptides derived
XX from the Wilm's tumour protein Wt1 and methods for their use in treating
XX malignant diseases. Peptides derived from both the murine and human Wt1
XX proteins are provided. The human Wt1 gene is found on chromosome 11p13,
XX and the protein was shown to be a zinc finger transcription factor. The
XX immunogenic peptides of the invention are particularly useful in the
XX diagnosis and treatment of cancer and leukaemia. The present sequence is
XX a polypeptide described in the exemplification of the invention
XX
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCL 9
DB 1 NAPYLPSCL 9

XX WO200162920-A2.
PN
XX
XX 30-AUG-2001.
XX
XX 22-FEB-2001; 2001WO-US005702.
PF
XX
XX 22-FEB-2000; 2000US-0184070P.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Cheever MA, Gaiger A;
PI
XX
XX WPI; 2001-648218/74.
DR
XX
XX Composition for the treatment of mesothelioma comprises specific peptides
PT i.e. Wilms' tumor antigen polypeptide derived antigenic fragments.
PT
XX
XX Claim 1; Page 245; 242pp; English.
PS
XX
XX The invention relates to the use of a composition comprising at least a
CC first isolated peptide, of between 9 and 40 amino acids or a first
CC nucleic acid, encoding the peptide, in the manufacture of a medicament
CC for treating or preventing mesothelioma. The peptides are antigenic
CC peptides derived from the Wilms' tumour protein Wt1. The composition is
CC useful for the treatment of mesothelioma, Wilms' tumour, preferably
CC pleural mesothelioma and other Wt1 associated malignancies e.g. leukaemia
CC (including acute myeloid leukaemia, ALL, chronic myeloid leukaemia, CML,
CC acute lymphocytic leukaemia, ALL, and childhood ALL), myelodysplastic
CC syndromes, myeloproliferative syndromes and cancers (e.g. breast,
CC testicular, prostate, lung and ovarian) in mammals, preferably humans.
CC The present sequence is an antigenic peptide of the invention derived
CC from mouse Wt1
XX
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSC 9
| | | | | | | |
Db 1 NAPYLPSC 9

RESULT 6
AAU68728
ID AAU68728 standard; peptide; 9 AA.
XX
XX AAU68728;
AC
XX 16-JAN-2002 (first entry)
DT
XX
XX Human Wilms' tumour protein, Wt1, antigenic peptide #123.
DE
XX
XX Human; Wilms' tumour; Wt1; pleural mesothelioma; antigen; leukaemia;
KW acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML;
KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
KW myeloproliferative syndrome; cancer; cytostatic.
XX
XX Homo sapiens.
OS
XX
XX WO200162920-A2.
PN
XX
XX 30-AUG-2001.
PD
XX
XX 22-FEB-2001; 2001WO-US005702.
PF
XX
XX 22-FEB-2000; 2000US-0184070P.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Cheever MA, Gaiger A;
PI

XX WO200162920-A2.
PN
XX
XX 30-AUG-2001.
XX
XX 22-FEB-2001; 2001WO-US005702.
PF
XX
XX 22-FEB-2000; 2000US-0184070P.
PR
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Cheever MA, Gaiger A;
PI
XX
XX WPI; 2001-648218/74.
DR
XX
XX Composition for the treatment of mesothelioma comprises specific peptides
PT i.e. Wilms' tumor antigen polypeptide derived antigenic fragments.
PT
XX
XX Claim 1; Page 245; 242pp; English.
PS
XX
XX The invention relates to the use of a composition comprising at least a
CC first isolated peptide, of between 9 and 40 amino acids or a first
CC nucleic acid, encoding the peptide, in the manufacture of a medicament
CC for treating or preventing mesothelioma. The peptides are antigenic
CC peptides derived from the Wilms' tumour protein Wt1. The composition is
CC useful for the treatment of mesothelioma, Wilms' tumour, preferably
CC pleural mesothelioma and other Wt1 associated malignancies e.g. leukaemia
CC (including acute myeloid leukaemia, ALL, chronic myeloid leukaemia, CML,
CC acute lymphocytic leukaemia, ALL, and childhood ALL), myelodysplastic
CC syndromes, myeloproliferative syndromes and cancers (e.g. breast,
CC testicular, prostate, lung and ovarian) in mammals, preferably humans.
CC The present sequence is an antigenic peptide of the invention derived
CC from mouse Wt1
XX
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSC 9
| | | | | | | |
Db 1 NAPYLPSC 9

RESULT 5
AAU68866
ID AAU68866 standard; peptide; 9 AA.
XX
XX AAU68866;
AC
XX 16-JAN-2002 (first entry)
DT
XX
XX Mouse Wilms' tumour protein, Wt1, antigenic peptide #35.
DE
XX
XX Mouse; Wilms' tumour; Wt1; pleural mesothelioma; antigen; leukaemia;
KW acute myeloid leukaemia; AML; chronic myeloid leukaemia; CML;
KW acute lymphocytic leukaemia; ALL; myelodysplastic syndromes;
KW myeloproliferative syndrome; cancer; cytostatic.
XX
XX Mus musculus.
OS

```
XX WPI; 2001-648218/74.
XX Composition for the treatment of mesothelioma comprises specific peptides
XX i.e. Wilms' tumor antigen polypeptide derived antigenic fragments.
XX Claim 1; Page 224; 242pp; English.
XX The invention relates to the use of a composition comprising at least a
XX first isolated peptide, of between 9 and 40 amino acids or a first
XX nucleic acid, encoding the peptide, in the manufacture of a medicament
XX for treating or preventing mesothelioma. The peptides are antigenic
XX peptides derived from the Wilms' tumour protein WT1. The composition is
XX useful for the treatment of mesothelioma, Wilms' tumour, preferably
XX pleural mesothelioma and other WT1 associated malignancies e.g. leukaemia
XX (including acute myeloid leukaemia, AML, chronic myeloid leukaemia, CML,
XX acute lymphocytic leukaemia, ALL, and childhood ALL), myelodysplastic
XX syndromes, myeloproliferative syndromes and cancers (e.g. breast,
XX testicular, prostate, lung and ovarian) in mammals, preferably humans.
XX The present sequence is an antigenic peptide of the invention derived
XX from human WT1
XX Sequence 9 AA;
XX Query Match 100.0%; Score 52; DB 4; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NAPYLPSCSL 9
DB 1 NAPYLPSCSL 9
XX
XX RESULT 7
XX ABG33336
XX ID ABG333336 standard; peptide; 9 AA.
XX AC ABG333336;
XX DT 15-JUL-2002 (first entry)
XX DE Mouse WT1 immunogenic peptide #33.
XX KW Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response.
XX OS Mus musculus.
XX PN WO200228414-A1.
XX PD 11-APR-2002.
XX PF 03-OCT-2001; 2001WO-US031139.
XX PR 06-OCT-2000; 2000US-00684361.
XX PR 09-OCT-2000; 2000US-00685830.
XX PR 15-FEB-2001; 2001US-00785019.
XX PR 24-AUG-2001; 2001US-00938864.
XX PA (CORI-) CORIXA CORP.
XX PI GAIGER A.
XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX DR WPI; 2002-352217/38.
XX
XX Query Match 100.0%; Score 52; DB 5; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NAPYLPSCSL 9
DB 1 NAPYLPSCSL 9
XX
XX RESULT 8
XX ABG33198
XX ID ABG33198 standard; peptide; 9 AA.
XX AC ABG33198;
XX DT 15-JUL-2002 (first entry)
XX DE Human WT1 immunogenic peptide #121.
XX KW Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response.
XX OS Homo sapiens.
XX PN WO200228414-A1.
XX PD 11-APR-2002.
XX PF 03-OCT-2001; 2001WO-US031139.
XX PR 06-OCT-2000; 2000US-00684361.
XX PR 09-OCT-2000; 2000US-00685830.
XX PR 15-FEB-2001; 2001US-00785019.
XX PR 24-AUG-2001; 2001US-00938864.
XX PA (CORI-) CORIXA CORP.
XX PI GAIGER A.
XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
XX PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX DR WPI; 2002-352217/38.
XX
XX Query Match 100.0%; Score 52; DB 5; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NAPYLPSCSL 9
DB 1 NAPYLPSCSL 9
XX
XX RESULT 9
XX ADB67484
XX ID ADB67484 standard; peptide; 9 AA.
```

XX AC ADB67484;
 XX DT 04-DEC-2003 (first entry)
 XX DE Mouse WT1 peptide binding mouse MHC class I Db #4.
 XX KW Mouse; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;
 KW antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
 KW leukaemia; antigen.
 XX OS Mus musculus.
 XX PN US2003072767-A1.
 XX PD 17-APR-2003.
 XX PF 24-AUG-2001; 2001US-00938864.
 XX PR 30-SEP-1998; 98US-00164223.
 XX PR 25-MAR-1999; 99US-00276484.
 XX PR 06-OCT-2000; 2000US-00684361.
 XX PR 09-OCT-2000; 2000US-00685830.
 XX PR 15-FEB-2001; 2001US-00785019.
 XX PA (GAIG/) GAIGER A.
 PA (MCNE/) MCNEILL P D.
 PA (SMIT/) SMITHGALL M.
 PA (MOUL/) MOULTON G.
 PA (VEDV/) VEDVICK T S.
 PA (SLEA/) SLEATH P R.
 PA (MOSS/) MOSSMAN S.
 PA (EVAN/) EVANS L.
 PA (SPIE/) SPIES A G.
 PA (BOYD/) BOYDSTON J.
 XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
 XX WPI; 2003-605957/57.
 XX Novel Wilms tumor polynucleotides encoding WT1 polypeptides, useful for
 PT detecting the presence of cancer in a patient, and in pharmaceutical
 PT compositions, e.g. vaccines, for treating cancers e.g. leukemia.
 XX Example 4; Page 54; 197pp; English.
 XX The invention relates to an isolated Wilm tumour (WT1) polynucleotide
 CC comprising a full length protein, truncated protein, mutated protein or
 CC fusion protein. Also included are the encoded WT1 proteins, expression
 CC vectors, host cells, antibodies, detecting the presence of a cancer in a
 CC patient by contacting a biological sample with a binding agent that binds
 CC to a WT1 protein, an oligonucleotide that hybridises to a WT1
 CC polynucleotide, stimulating and/or expanding T cells specific for a
 CC tumour protein by contacting T cells with the WT1 polynucleotide, the WT1
 CC protein or antigen-presenting cells that express the WT1 protein, a
 CC composition (C1) comprising physiologically acceptable carriers and
 CC immunostimulants as first component, and a second component selected from
 CC the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen
 CC presenting cells that express the WT1 protein, inhibiting the
 CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
 CC cells isolated from a patient with the WT1 polynucleotide, the WT1
 CC protein or antigen presenting cells that express the WT1 protein, such
 CC that T cell proliferate, administering the proliferated T cells to the
 CC patient, and thus inhibiting the development of a cancer in the patient)
 CC and a composition (C2) comprising a WT1 polypeptide resuspended in a
 CC buffer comprising at least 1-3 sugars selected from trehalose, maltose,
 CC sucrose, fructose and glucose, at a concentration of 7-13%, and
 CC optionally ethanolamine, cysteine and Polysorbate-80, or WT1 polypeptide
 CC and MPL-SE or Enhanzyn). Also disclosed as anew are polypeptides
 CC comprising a variant of an immunogenic portion of WT1 polypeptide. C1 is
 CC useful for stimulating immune response in a patient, and for treating
 CC cancer in a patient. The oligonucleotide is also useful for determining

CC the presence of a cancer in a patient. The WT1 polynucleotide and the WT1
 CC protein are useful in pharmaceutical compositions, e.g. vaccines. the WT1
 CC protein is useful as marker to indicate the presence or absence of a
 CC cancer. C1 is useful for inhibiting the development of a malignant
 CC disease in a patient, for preventing and treating metastatic diseases
 CC e.g. leukaemia and cancer, and for removing tumour cells from a
 CC biological sample. Ab (binding agent for the WT1 protein) is useful for
 CC detecting the presence of cancer in a patient. The present sequence is a
 XX mouse WT1 antigenic peptide.
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 52; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NAPYLPSCL 9
 Db 1 NAPYLPSCL 9
 RESULT 10
 ADB67346
 ID ADB67346 standard; peptide; 9 AA.
 XX AC ADB67346;
 XX DT 04-DEC-2003 (first entry)
 XX DE Human WT1 HLA A24-binding peptide #5.
 XX KW Human; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;
 KW antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
 KW leukaemia; antigen.
 XX OS Homo sapiens.
 XX PN US2003072767-A1.
 XX PD 17-APR-2003.
 XX PF 24-AUG-2001; 2001US-00938864.
 XX PR 30-SEP-1998; 98US-00164223.
 XX PR 25-MAR-1999; 99US-00276484.
 XX PR 06-OCT-2000; 2000US-00684361.
 XX PR 09-OCT-2000; 2000US-00685830.
 XX PR 15-FEB-2001; 2001US-00785019.
 XX PA (GAIG/) GAIGER A.
 PA (MCNE/) MCNEILL P D.
 PA (SMIT/) SMITHGALL M.
 PA (MOUL/) MOULTON G.
 PA (VEDV/) VEDVICK T S.
 PA (SLEA/) SLEATH P R.
 PA (MOSS/) MOSSMAN S.
 PA (EVAN/) EVANS L.
 PA (SPIE/) SPIES A G.
 PA (BOYD/) BOYDSTON J.
 XX PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedvick TS;
 PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
 XX WPI; 2003-605957/57.
 XX Novel Wilms tumor polynucleotides encoding WT1 polypeptides, useful for
 PT detecting the presence of cancer in a patient, and in pharmaceutical
 PT compositions, e.g. vaccines, for treating cancers e.g. leukemia.
 XX Example 4; Page 24; 197pp; English.
 XX The invention relates to an isolated Wilm tumour (WT1) polynucleotide
 CC comprising a full length protein, truncated protein, mutated protein or

CC fusion protein. Also included are the encoded WT1 proteins, expression
 CC vectors, host cells, antibodies, detecting the presence of a cancer in a
 CC patient by contacting a biological sample with a binding agent that binds
 CC to a WT1 protein, an oligonucleotide that hybridizes to a WT1
 CC polynucleotide, stimulating and/or expanding T cells specific for a
 CC tumour protein by contacting T cells with the WT1 polynucleotide, the WT1
 CC protein or antigen-presenting cells that express the WT1 protein, a
 CC composition (C1) comprising physiologically acceptable carriers and
 CC immunostimulants as first component, and a second component selected from
 CC the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen
 CC presenting cells that express the WT1 protein), inhibiting the
 CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
 CC cells isolated from a patient with the WT1 polynucleotide, the WT1
 CC protein or antigen presenting cells that express the WT1 protein, such
 CC that T cell proliferate, administering the proliferated T cells to the
 CC patient, and thus inhibiting the development of a cancer in the patient)
 CC and a composition (C2) comprising a WT1 polypeptide resuspended in a
 CC buffer comprising at least 1-3 sugars selected from trehalose, maltose,
 CC sucrose, fructose and glucose, at a concentration of 7-13%, and
 CC optionally ethanolamine, cysteine and Polysorbate-80, or WT1 polypeptide
 CC and MPL-SE or Enhanzyn). Also disclosed as anew are polypeptides
 CC comprising a variant of an immunogenic portion of WT1 polypeptide. C1 is
 CC useful for stimulating immune response in a patient, and for treating
 CC cancer in a patient. The oligonucleotide is also useful for determining
 CC the presence of a cancer in a patient. The WT1 polynucleotide and the WT1
 CC protein are useful in pharmaceutical compositions, e.g. vaccines. the WT1
 CC protein is useful as marker to indicate the presence or absence of a
 CC cancer. C1 is useful for inhibiting the development of a malignant
 CC disease in a patient, for preventing and treating metastatic diseases
 CC e.g. leukaemia and cancer, and for removing tumour cells from a
 CC biological sample. Ab (binding agent for the WT1 protein) is useful for
 CC detecting the presence of cancer in a patient. The present sequence is a
 CC human WT1 antigenic peptide.

XX Sequence 9 AA;

Query Match 100.0%; Score 52; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0;
 Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 1 NAPYLPSCL 9
 DB 1 NAPYLPSCL 9

RESULT 11

ADJ80579
 ID ADJ80579 standard; peptide; 9 AA.

XX AC ADJ80579;

XX DT 06-MAY-2004 (first entry)

XX DE Wilm's tumor antigen immunogenic peptide #129.

XX KW cytostatic; gene therapy; vaccine; Wilm's tumor antigen; WT1; cancer;
 XX LW leukemia.

XX OS Homo sapiens.

XX PN WO2003037060-A2.

XX PD 08-MAY-2003.

XX PF 30-OCT-2002; 2002WO-US035194.

XX PR 30-OCT-2001; 2001US-00002603.

XX PR 16-APR-2002; 2002US-00125635.

XX PR 12-JUL-2002; 2002US-00195835.

XX PR 16-SEP-2002; 2002US-00244830.

XX PA (CORI-) CORIXA CORP.

XX PA (GAIG/) GAIGER A.

XX Gaiger A, Mcneill PD, Jaya N, Carter D;
 PI WPI; 2003-430453/40.

XX DT New isolated polypeptide for diagnosing, preventing or treating malignant
 XX diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a
 XX Wilm's tumor antigen.

XX PS Disclosure; SEQ ID NO 144; 371pp; English.

XX CC The invention relates to an isolated polypeptide comprising an
 CC immunogenic portion of a Wilm's tumor antigen, or its variant that
 CC differs in one or more substitutions, deletions, additions and/or
 CC insertions, such that the ability of the variant to react with WT1-
 CC specific antisera and/or T-cell lines or clones is not substantially
 CC diminished. The composition and methods are useful in diagnosing,
 CC preventing or treating malignant diseases, such as cancer or leukemia.
 CC This sequence represents a peptide of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCL 9

DB 1 NAPYLPSCL 9

RESULT 12

ADJ80717

ID ADJ80717 standard; peptide; 9 AA.

XX AC ADJ80717;

XX DT 06-MAY-2004 (first entry)

XX DE Wilm's tumor antigen immunogenic peptide #267.

XX KW cytostatic; gene therapy; vaccine; Wilm's tumor antigen; WT1; cancer;
 XX LW leukemia.

XX OS Homo sapiens.

XX PN WO2003037060-A2.

XX PD 08-MAY-2003.

XX PF 30-OCT-2002; 2002WO-US035194.

XX PR 30-OCT-2001; 2001US-00002603.

XX PR 16-APR-2002; 2002US-00125635.

XX PR 12-JUL-2002; 2002US-00195835.

XX PR 16-SEP-2002; 2002US-00244830.

XX PA (CORI-) CORIXA CORP.

XX PA (GAIG/) GAIGER A.

XX PI Gaiger A, Mcneill PD, Jaya N, Carter D;
 XX WPI; 2003-430453/40.

XX DT New isolated polypeptide for diagnosing, preventing or treating malignant
 XX diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a
 XX Wilm's tumor antigen.

XX PS Disclosure; SEQ ID NO 282; 371pp; English.

XX CC The invention relates to an isolated polypeptide comprising an
 XX immunogenic portion of a Wilm's tumor antigen, or its variant that
 XX differs in one or more substitutions, deletions, additions and/or

XX CC

CC insertions, such that the ability of the variant to react with WT1-
 CC specific antisera and/or T-cell lines or clones is not substantially
 CC diminished. The composition and methods are useful in diagnosing,
 CC preventing or treating malignant diseases, such as cancer or leukemia.
 CC This sequence represents a peptide of the invention.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCSCL 9
 |||||

Db 1 NAPYLPSCSCL 9
 |||||

RESULT 13
 ADJ83637
 ID ADJ83637 standard; peptide; 9 AA.
 AC ADJ83637;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Murine WT1 (Wilms tumour) immunogenic peptide - SEQ ID 282.
 XX
 KW immune response; WT1; Wilms tumour; immunostimulant; cytostatic; vaccine;
 KW malignant disease; leukaemia; cancer; murine; mouse.
 XX
 OS Mus musculus.
 XX
 PN US2003235557-A1.
 XX
 PD 25-DEC-2003.
 XX
 PF 16-SEP-2002; 2002US-00244830.
 XX
 PR 30-SEP-1998; 98US-00164223.
 PR 25-MAR-1999; 99US-00276484.
 PR 06-OCT-2000; 2000US-00684361.
 PR 09-OCT-2000; 2000US-00685830.
 PR 15-FEB-2001; 2001US-00785019.
 PR 24-AUG-2001; 2001US-00938864.
 PR 30-OCT-2001; 2001US-00002603.
 PR 16-APR-2002; 2002US-00125635.
 PR 12-JUL-2002; 2002US-00195835.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Gaiger A, Cheever MA;
 XX
 DR WPI; 2004-070542/07.
 XX
 PT Inducing an immune response in an animal, useful for treating or
 PT preventing cancer, comprises administering a composition comprising a
 PT viral vector comprising an immunogenic portion of a WT1 polynucleotide.
 XX
 PS Example 4; SEQ ID NO 282; 229pp; English.

XX
 CC The invention relates to a novel method for inducing an immune response
 CC in an animal which involves administering a first and a second
 CC composition comprising a first and a second viral vector, respectively,
 CC each having at least an immunogenic portion of a WT1 (Wilms tumour)
 CC polynucleotide operably linked to an expression control sequence. The
 CC method of the invention has immunostimulant and cytostatic applications
 CC and may be useful for generating or enhancing an immune response to WT1,
 CC possibly via the production of a vaccine, as well as for preventing
 CC and/or treating malignant diseases such as leukaemia and cancer. The
 CC current sequence is that of the murine WT1 immunogenic peptide of the
 CC invention.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCSCL 9
 |||||

Db 1 NAPYLPSCSCL 9
 |||||

RESULT 14
 ADJ83499
 ID ADJ83499 standard; peptide; 9 AA.
 AC ADJ83499;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human WT1 (Wilms tumour) immunogenic peptide - SEQ ID 144.
 XX
 KW immune response; WT1; Wilms tumour; immunostimulant; cytostatic; vaccine;
 KW malignant disease; leukaemia; cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003235557-A1.
 XX
 PD 25-DEC-2003.
 XX
 PF 16-SEP-2002; 2002US-00244830.
 XX
 PR 30-SEP-1998; 98US-00164223.
 PR 25-MAR-1999; 99US-00276484.
 PR 06-OCT-2000; 2000US-00684361.
 PR 09-OCT-2000; 2000US-00685830.
 PR 15-FEB-2001; 2001US-00785019.
 PR 24-AUG-2001; 2001US-00938864.
 PR 30-OCT-2001; 2001US-00002603.
 PR 16-APR-2002; 2002US-00125635.
 PR 12-JUL-2002; 2002US-00195835.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Gaiger A, Cheever MA;
 XX
 DR WPI; 2004-070542/07.
 XX
 PT Inducing an immune response in an animal, useful for treating or
 PT preventing cancer, comprises administering a composition comprising a
 PT viral vector comprising an immunogenic portion of a WT1 polynucleotide.
 XX
 PS Example 4; SEQ ID NO 144; 229pp; English.

XX
 CC The invention relates to a novel method for inducing an immune response
 CC in an animal which involves administering a first and a second
 CC composition comprising a first and a second viral vector, respectively,
 CC each having at least an immunogenic portion of a WT1 (Wilms tumour)
 CC polynucleotide operably linked to an expression control sequence. The
 CC method of the invention has immunostimulant and cytostatic applications
 CC and may be useful for generating or enhancing an immune response to WT1,
 CC possibly via the production of a vaccine, as well as for preventing
 CC and/or treating malignant diseases such as leukaemia and cancer. The
 CC current sequence is that of the murine WT1 immunogenic peptide of the
 CC invention.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCSCL 9
 |||||

CC malignant diseases, e.g. cancer. The compositions may be used as markers
 CC for the progression of cancer. The present sequence is a mouse WT1
 CC polypeptide-immunogenic peptide.
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 52; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NAYLPSCL 9
 Db 1 NAYLPSCL 9
 Search completed: May 5, 2006, 16:19:11
 Job time : 186 secs

Db 1 NAYLPSCL 9
 RESULT 15
 ADL57525 standard; peptide; 9 AA.
 ADL57525;
 20-MAY-2004 (first entry)
 Mouse WT-1 MHC class I Db-binding peptide #6.
 Mouse; Wilms' tumour; WT1; cancer; cytostatic; immunogen; antigen;
 vaccine; T-cell; MHC; Major Histocompatibility Complex; HLA-A2;
 human leukocyte antigen; Ral2; HIS tag; twin arginine translocator; TAT;
 malignant disease.
 Mus musculus.
 US2003215458-A1.
 20-NOV-2003.
 30-OCT-2002; 2002US-00286333.
 30-SEP-1998; 98US-00164223.
 25-MAR-1999; 99US-00276484.
 06-OCT-2000; 2000US-00684361.
 09-OCT-2000; 2000US-00685830.
 15-FEB-2001; 2001US-00785019.
 24-AUG-2001; 2001US-00938864.
 30-OCT-2001; 2001US-00002603.
 16-APR-2002; 2002US-00125635.
 12-JUL-2002; 2002US-00195835.
 16-SEP-2002; 2002US-00244830.
 (CORI-) CORIXA CORP.
 Gaiger A, Mcneill PD, Jaya N;
 WPI; 2004-021827/02.
 New polypeptides and polynucleotides useful for generating or enhancing
 an immune response to Wilms' tumor, or for treating and/or preventing
 malignant diseases, e.g. cancer.
 Example 4; SEQ ID NO 282; 259pp; English.
 The invention relates to an isolated polypeptide comprising an
 immunogenic portion of a Wilms' tumour antigen (WT1), or their variants
 that differs in substitution(s), deletion(s), addition(s) and/or
 insertion(s), where ability of the variant to react with WT1-specific
 antisera and/or T-cell lines or clones is not substantially diminished.
 Also included are a fusion protein comprising at least one WT1
 polypeptide, an isolated polynucleotide encoding the fusion protein, a
 composition comprising a WT1 polypeptide in combination with a
 pharmaceutical carrier or excipient, a vaccine comprising a WT1
 polypeptide in combination with a non-specific immune response enhancer,
 an expression vector comprising the polynucleotide operably linked to an
 expression control sequence and a host cell transformed or transfected
 with the expression vector. The immunogenic portion of the WT1
 polypeptide has been modified such that the ability of the immunogenic
 portion to bind to an MHC (Major Histocompatibility Complex) molecule or
 to HLA-A2 is increased relative to that of the immunogenic portion. The
 WT1 polypeptide may comprise a Wilms' tumour antigen having a deletion of
 a proline rich region at amino acid positions 54-68 of the Wilms' tumour
 antigen. The fusion partner is selected from Ral2, protein D, LYTA, a HIS
 tag, a targeting signal capable of directing a polypeptide to the
 endosomal/lysosomal compartment, twin arginine translocator (TAT), and
 truncated twin arginine translocator. The polypeptide, polynucleotide or
 compositions comprising them may be used for generating or enhancing an
 immune response to Wilms' tumour, and for treating and/or preventing

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 16:19:31 ; Search time 39 Seconds
(without alignments)
22.204 Million cell updates/sec

Title: US-09-684-361C-144
Perfect score: 52
Sequence: 1 NAPYLPSCCL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	52	100.0	448	2 S33926	Wilms' tumor prote
2	52	100.0	449	2 A38080	Wilms' tumor suscep
3	52	100.0	449	2 A39692	Wilms' tumor prote
4	41	78.8	410	2 JC5046	Wilms' tumor suppr
5	39	75.0	432	2 T23343	hypothetical prote
6	38	73.1	577	2 C71342	probable CTP synth
7	37	71.2	113	2 AG2081	thioredoxin (impor
8	37	71.2	188	2 JU0451	hypothetical 21K p
9	37	71.2	188	2 I59116	myc protein - huma
10	37	71.2	188	2 A29867	hypothetical 20K p
11	37	71.2	188	2 I79500	myc protein - huma
12	37	71.2	438	2 A47702	glucan 1,3-beta-gl
13	37	71.2	438	2 T52149	beta-glucanase [im
14	37	71.2	815	2 T00264	high carbon dioxid
15	36	69.2	144	2 A12108	hypothetical prote
16	36	69.2	157	2 A25964	thyroglobulin - ra
17	36	69.2	257	2 I55488	25-hydroxyvitamin
18	36	69.2	513	1 A47436	1,25-dihydroxyvita
19	36	69.2	514	2 S60033	25-hydroxyvitamin
20	36	69.2	514	2 A45228	25-hydroxyvitamin
21	36	69.2	594	2 A49804	cellular Hsp70 hom
22	35	67.3	77	2 A11306	hypothetical prote
23	35	67.3	77	2 A11678	hypothetical prote
24	35	67.3	209	2 D95037	hypothetical prote
25	35	67.3	209	2 G97907	4-hydroxy-2-oxoglu
26	35	67.3	280	2 S50369	probable membrane
27	35	67.3	348	2 T07659	cyclin al-type, mi
28	35	67.3	420	2 AG2473	hypothetical prote
29	35	67.3	461	2 JC4556	alcaligin synthesi

30	35	67.3	470	2 T31602	hypothetical prote
31	35	67.3	730	2 JH0798	fasciclin IV precu
32	35	67.3	2767	1 UIHU	thyroglobulin prec
33	35	67.3	2769	1 UIBO	thyroglobulin prec
34	34	65.4	122	2 I46994	corticotropin rele
35	34	65.4	145	2 T15608	hypothetical prote
36	34	65.4	153	2 C83004	probable rRNA meth
37	34	65.4	194	2 T29516	hypothetical prote
38	34	65.4	214	2 T44701	probable integral
39	34	65.4	253	2 S09215	erythromycin resis
40	34	65.4	294	2 H96719	homeobox gene 13 p
41	34	65.4	349	2 T20912	hypothetical prote
42	34	65.4	359	1 OKKWC1	protein kinase (EC
43	34	65.4	359	2 T21211	hypothetical prote
44	34	65.4	426	1 BVECTD	lysine 6-monooxyge
45	34	65.4	445	2 T44482	lysine 6-monooxyge

ALIGNMENTS

RESULT 1

S33926
Wilms' tumor protein WT1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-May-1996
C:Accession: S33926
R:Sharma, P.M.; Yang, X.; Bowman, M.; Roberts, V.; Sukumar, S.
Cancer Res. 52, 6407-6412, 1992
A>Title: Molecular cloning of rat Wilms' tumor complementary DNA and a study of messenger RNA expression
A:Reference number: S33926; MUID:93046155; PMID:1330293
A:Accession: S33926
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-448 <SHA>
C:Genetics:
A:Gene: WT1
C:Keywords: tumor suppressor

Query Match 100.0%; Score 52; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCCL 9
DB 129 NAPYLPSCCL 137

RESULT 2

A38080
Wilms tumor susceptibility protein WT1 - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C:Accession: A38080; S08273; A34673; I38504; I52811; I58315; A56411; S26286
R:Gesler, M.; Konig, A.; Bruns, G.A.
Genomics 12, 807-813, 1992
A>Title: The genomic organization and expression of the WT1 gene.
A:Reference number: A38080; MUID:92241883; PMID:1572653
A:Accession: A38080
A:Molecule type: DNA
A:Residues: 1-449 <GES1>
A:Cross-references: UNIPARC:UPI000017C420; GB:X61631; GB:S99414; NID:937981; PIDN:CAA43
A>Note: It is uncertain whether Met-1 is the initiator or whether translation is initiated
A>Note: sequence extracted from NCBI backbone (NCBIN:99414, NCBIN:99422, NCBIN:99479, N
A>Note: the sequence in GenBank entry HSWTGEEX1, release 113.0, PIDN:CAA43819.1 differs
R:Gesler, M.; Poustka, A.; Cavenee, W.; Neve, R.L.; Orkin, S.H.; Bruns, G.A.P.
Nature 343, 774-778, 1990
A>Title: Homozygous deletion in Wilms tumours of a zinc-finger gene identified by chromo
A:Reference number: S08273; MUID:90158822; PMID:2154702
A:Accession: S08273
A:Molecule type: mRNA
A:Residues: 'SRQRPFGALRNPTACPLPFPSPPTHTSPTRAGTAQAQAPRRLLAA1LDFLLQLQDPASTCVPPEASQH

A;Cross-references: UNIPARC:UPI000016B316; EMBL:X51630; NID:g37977; PIDN:CAA35956.1; PID:R;Call, K.M.; Glaser, T.; Ito, C.Y.; Buckler, A.J.; Pelletier, J.; Haber, D.A.; Rose, E. Cell 60, 509-520, 1990

A;Title: Isolation and characterization of a zinc finger polypeptide gene at the human c

A;Reference number: A34673; MUID:90150277; PMID:2154335

A;Accession: A34673

A;Molecule type: mRNA

A;Residues: 85-249, 267-364, 'F', 366-386, 'T', 388-407, 411-449 <CAL>

A;Cross-references: UNIPARC:UPI0000147983; GB:M30393; NID:g340381; PIDN:AAA36910.1; PID:R;Haber, D.A.; Sohn, R.L.; Buckler, A.J.; Pelletier, J.; Call, K.M.; Housman, D.E. Proc. Natl. Acad. Sci. U.S.A. 88, 9618-9622, 1991

A;Title: Alternative splicing and genomic structure of the Wilms tumor gene WTL.

A;Reference number: A56411; MUID:92052142; PMID:1658787

A;Contents: annotation; alternative splicing

A;Phelan, S.A.; Lindberg, C.; Call, K.M. Cell Growth Differ. 5, 677-686, 1994

A;Title: Wilms' tumor gene, WTL, mRNA is down-regulated during induction of erythroid an

A;Reference number: I38504; MUID:94368704; PMID:8086342

A;Accession: I38504

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-18 <PHE>

A;Cross-references: UNIPARC:UPI00000052B; EMBL:U06486; NID:g473563; PIDN:AAAG2865.1; PID:R;Pelletier, J.; Bruening, W.; Kashtan, C.E.; Maurer, J.C.; Manivel, J.C.; Striegel, J.E. Cell 67, 437-447, 1991

A;Title: Germ-line mutations in the Wilms' tumor suppressor gene are associated with abnc

A;Reference number: I52811; MUID:92005721; PMID:1655284

A;Accession: I52811

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 355-365, 'H', 367-377 <PEL>

A;Cross-references: UNIPARC:UPI000011DDFA; GB:S61513; NID:g237599; PIDN:AAB20109.1; PID:R;Hamilon, T.B.; Barilla, K.C.; Romaniuk, P.J. Nucleic Acids Res. 23, 277-284, 1995

A;Title: High affinity binding sites for the Wilms' tumour suppressor protein WTL.

A;Reference number: I58315; MUID:95166649; PMID:7862533

A;Accession: I58315

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 'MGHHHHHHHHSHGIEGRHM', 301-364, 'F', 366-386, 'T', 388-407, 411-449 <HAM>

A;Cross-references: UNIPARC:UPI0000072BDE; GB:S75264; NID:g896246; PIDN:AAB33443.1; PID:R;Note: this sequence is engineered

C;Genetics:

A;Gene: GDB:WTL

A;Cross-references: GDB:120496; OMIM:194070

A;Map position: 11p13-11p13

A;Introns: 148/1; 189/1; 223/2; 249/2; 266/2; 298/3; 349/1; 379/1; 410/1

A;Note: mRNA transcripts containing both alternatively spliced regions are the most abun

C;Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zinc finger

F;1-449/Product: Wilms tumor susceptibility protein WTL, splice form 1 #status Predicted

F;1-407,411-449/Product: Wilms tumor susceptibility protein WTL, splice form 4 #status P

F;1-249,267-449/Product: Wilms tumor susceptibility protein WTL, splice form 3 #status P

F;1-249,267-449/Product: Wilms tumor susceptibility protein WTL, splice form 2 #

Query Match 100.0%; Score 52; DB 2; Length 449;

Best Local Similarity 100.0%; Pred. No. 0.075;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPYLPSCUL 9

Db 130 NAPYLPSCUL 138

RESULT 3

A39692

Wilms' tumor protein analog, WTL - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 16-Feb-1997

C;Accession: A39692

R;Buckler, A.J.; Pelletier, J.; Haber, D.A.; Glaser, T.; Housman, D.E. Mol. Cell. Biol. 11, 1707-1712, 1991

A;Title: Isolation, characterization, and expression of the murine Wilms' tumor gene (WTL

A;Reference number: A39692; MUID:91141522; PMID:1671709

A;Accession: A39692

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-449 <BUC>

C;Cross-references: UNIPARC:UPI0000147984; GB:M55512

C;Keywords: alternative splicing; DNA binding; transcription regulation; tumor suppressor

Query Match 100.0%; Score 52; DB 2; Length 449;

Best Local Similarity 100.0%; Pred. No. 0.075;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPYLPSCUL 9

Db 130 NAPYLPSCUL 138

RESULT 4

JC5046

Wilms' tumor suppressor protein - African clawed frog

N;Alternate names: WTL

C;Species: Xenopus laevis (African clawed frog)

C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004

C;Accession: JC5046

R;Semba, K.; Saito-Ueno, R.; Takayama, G.; Kondo, M. Gene 175, 167-172, 1996

A;Title: cDNA cloning and its pronephros-specific expression of the Wilms' tumor suppress

A;Reference number: JC5046; MUID:97074667; PMID:8917094

A;Contents: testis

A;Accession: JC5046

A;Molecule type: mRNA

A;Residues: 1-410 <SEM>

A;Cross-references: UNIPROT:P79958; UNIPARC:UPI000017BFA3; DDBJ:D82051

C;Comment: This protein is involved in kidney morphogenesis.

C;Genetics:

A;Gene: wtl

Query Match 78.8%; Score 41; DB 2; Length 410;

Best Local Similarity 77.8%; Pred. No. 7;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPYLPSCUL 9

Db 111 NAPYLSNCL 119

RESULT 5

T23343

hypothetical protein K05C4.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T23343

R;Harris, B. submitted to the EMBL Data Library, November 1996

A;Reference number: Z19729

A;Accession: T23343

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-432 <WIL>

A;Cross-references: UNIPROT:Q9XU04; UNIPARC:UPI0000080AD7; EMBL:Z81564; PIDN:CAB04574.1;

A;Experimental source: clone K05C4

C;Genetics:

A;Gene: CESP:K05C4.4

A;Map position: 1

A;Introns: 33/1; 70/2; 132/3; 292/1; 330/3; 364/1

Query Match 75.0%; Score 39; DB 2; Length 432;

Best Local Similarity 75.0%; Pred. No. 17;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPYLPSC 8

Db 344 NFPYLPNC 351

RESULT 6

C71342
probable CTP synthase (pvrG) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: C71342
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: AV1250; MUID:98332770; PMID:9665876
A:Accession: C71342
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-577 <COL>
A:Cross-references: UNIPROT:O83327; UNIPARC:UPI0000132D88; GB:AE001210; GB:AE000520; NID
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0305
C:Superfamily: CTP synthase

Query Match 73.1%; Score 38; DB 2; Length 577;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 8

Db 180 PYLPSC 185
|||||

RESULT 7

AG2081
thioredoxin [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004
C:Accession: AG2081
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takarawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2081
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <KUR>
A:Cross-references: UNIPROT:Q8YUX6; UNIPARC:UPI000000CE367; GB:BA0000019; PIDN:BA073904.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2205

Query Match 71.2%; Score 37; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APYLPSC 8

Db 35 APYLPSC 41
|||||

RESULT 8

JU0451
hypothetical 21K protein (c-myc 5' region) - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JU0451
R:Argaut, C.; Rigoler, M.; Eladari, M.E.; Galibert, F.
Gene 97, 231-237, 1991
A:Title: Cloning and nucleotide sequence of the chimpanzee c-myc gene.
A:Reference number: JU0449; MUID:91153652; PMID:1999286

A:Accession: JU0451
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-188 <ARG>
A:Cross-references: UNIPROT:Q9SKK3; UNIPARC:UPI000006D15D; GB:M38057; NID:q176652; PIDN:

Query Match 71.2%; Score 37; DB 2; Length 188;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 9

Db 25 PYLPSC 31
|||||

RESULT 9

I59116
myc protein - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I59116
R:Finver, S.N.; Nishikura, K.; Finger, L.R.; Haluska, F.G.; Finan, J.; Nowell, P.C.; Cro
Proc. Natl. Acad. Sci. U.S.A. 85, 3052-3056, 1988
A:Title: Sequence analysis of the MYC oncogene involved in the t(8;14)(q24;q11) chromoso
A:Reference number: I59116; MUID:88203638; PMID:2834731
A:Accession: I59116
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-188 <RES>
A:Cross-references: UNIPROT:Q14901; UNIPARC:UPI000006E838; GB:M20605; NID:g188974; PIDN:

Query Match 71.2%; Score 37; DB 2; Length 188;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 9

Db 25 PYLPSC 31
|||||

RESULT 10

A29867
hypothetical 20K protein (myc 5' region) (Burkitt lymphoma) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A29867
R:Showe, L.C.; Moore, R.C.A.; Erikson, J.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 2824-2828, 1987
A:Title: MYC oncogene involved in a t(8;22) chromosome translocation is not altered in
A:Reference number: A29867; MUID:87204220; PMID:3033665
A:Accession: A29867
A:Molecule type: DNA
A:Residues: 1-188 <SHO>
A:Cross-references: UNIPROT:Q16591; UNIPROT:Q14901; UNIPARC:UPI0000179710

Query Match 71.2%; Score 37; DB 2; Length 188;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 9

Db 25 PYLPSC 31
|||||

RESULT 11

I79500
myc protein - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I79500
R:Finver, S.N.; Nishikura, K.; Finger, L.R.; Haluska, F.G.; Finan, J.; Nowell, P.C.; Cr
Proc. Natl. Acad. Sci. U.S.A. 85, 3052-3056, 1988
A:Title: Sequence analysis of the MYC oncogene involved in the t(8;14)(q24;q11) chromosom

A;Reference number: I59116; MUID:88203638; PMID:2834731
A;Accession: I79500
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-188 <RES>
A;Cross-references: UNIPROT:Q16591; UNIPARC:UPI000006D15D; GB:J03253; NID:gl88976; PIDN:

Query Match 71.2%; Score 37; DB 2; Length 188;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYPSPCL 9
DB 25 PWPSPCL 31

RESULT 12

A47702
glucan 1,3-beta-glucosidase (EC 3.2.1.58) - yeast (Candida albicans)
N;Alternate names: exo-beta-(1,3)-glucanase
C;Species: Candida albicans
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jun-2000
R;Chambers, R.S.; Broughton, M.J.; Cannon, R.D.; Carne, A.; Emerson, G.W.; Sullivan, P.A.
J. Gen. Microbiol. 139, 325-334, 1993
A;Title: An exo-beta-(1,3)-glucanase of Candida albicans: purification of the enzyme and
A;Reference number: A47702; MUID:93171875; PMID:8436950
A;Accession: A47702
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-438 <CHA>
A;Cross-references: UNIPARC:UPI0000178FB5; EMBL:X56556
A;Experimental source: ATCC 10261
A;Note: Sequence extracted from NCBI backbone (NCBIP:125650)
A;Gene: XOG
C;Superfamily: yeast glucan 1,3-beta-glucanase EXG1
C;Keywords: glycosidase; hydrolase

Query Match 71.2%; Score 37; DB 2; Length 438;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAYLPSC 8
DB 357 NAPIGSC 364

RESULT 13

T52149
beta-glucanase [imported] - yeast (Candida albicans)
C;Species: Candida albicans
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C;Accession: T52149
R;Taylor, K.; Harris, D.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z25985
A;Accession: T52149
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-438 <TAY>
A;Cross-references: UNIPARC:UPI0000069E78; EMBL:AL033497; PIDN:CAA21969.1
A;Experimental source: strain 1161; cosmid Ca49C10
C;Genetics:
A;Gene: xog1
A;Map position: 1
C;Superfamily: yeast glucan 1,3-beta-glucanase EXG1

Query Match 71.2%; Score 37; DB 2; Length 438;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAYLPSC 8

DB 357 NAPIGSC 364

RESULT 14

T00264
high carbon dioxide response protein 2 - Chlorococcum littorale
N;Alternate names: HCR2 protein
C;Species: Chlorococcum littorale
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T00264
R;Sasaki, T.; Kurano, N.; Miyachi, S.
Plant Cell Physiol. 39, 131-138, 1998
A;Title: Cloning and characterization of high-CO2-specific cDNAs from a marine microalga
A;Reference number: Z14135; MUID:98220314; PMID:9559558
A;Accession: T00264
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-815 <SAS>
A;Cross-references: UNIPROT:O22113; UNIPARC:UPI00000A46C2; EMBL:AB007993; NID:g2541871;

Query Match 71.2%; Score 37; DB 2; Length 815;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 APYLPSC 9
DB 786 APFMTCL 793

RESULT 15

AI2108
hypothetical protein all2424 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AI2108
R;Kneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,
N.; Kato, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genome Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-144 <KUR>
A;Cross-references: UNIPROT:O8YUC9; UNIPARC:UPI00000CE423; GB:BA000019; PIDN:BA074123.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all2424

Query Match 69.2%; Score 36; DB 2; Length 144;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APYLPSC 9
DB 12 APYLPSC 19

Search completed: May 5, 2006, 16:23:51
Job time : 41 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 16:16:16 ; Search time 229 Seconds
(without alignments)
27.728 Million cell updates/sec

Title: US-09-684-361C-144
Perfect score: 52
Sequence: 1 NAYPLPSCL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	249	2 Q6P138_HUMAN	Q6P138 homo sapien
2	52	100.0	429	2 Q4VXV5_HUMAN	Q4VXV5 homo sapien
3	52	100.0	432	2 Q4VXV6_HUMAN	Q4VXV6 homo sapien
4	52	100.0	448	1 WT1_RAT	P49952 rattus norv
5	52	100.0	449	1 WT1_HUMAN	P19544 homo sapien
6	52	100.0	449	1 WT1_MOUSE	P22561 mus musculu
7	52	100.0	449	1 WT1_PIG	O62651 sus scrofa
8	45	86.5	390	2 Q42223_TRASC	O42223 trachemys s
9	45	86.5	426	2 Q9W611_CYNPY	Q9W611 cynops pyrr
10	44	84.6	225	2 P87542_9CLOS	P87542 beet pseudo
11	44	84.6	554	2 Q80625_9CLOS	Q80625 cucumber ye
12	44	84.6	554	2 Q6VRA5_9CLOS	Q6VRA5 beet pseudo
13	44	84.6	555	2 Q5ICV4_9CLOS	Q5ICV4 blackberry
14	44	84.6	555	2 Q5FYX8_9CLOS	Q5FYX8 blackberry
15	44	84.6	555	2 Q5FYV1_9CLOS	Q5FYV1 blackberry
16	42	80.8	392	2 Q9IBF0_ANGJA	Q9IBF0 anguilla ja
17	41	78.8	407	2 P79958_XENLA	P79958 xenopus lae
18	41	78.8	409	2 Q1657_XENLA	Q1657 xenopus lae
19	40	76.9	954	2 Q7VGA9_HELHP	Q7VGA9 helicobacte
20	39	75.0	138	2 Q8TJY0_METAC	Q8TJY0 methanosaar
21	39	75.0	173	2 Q5YKQ0_CRYNE	Q5YKQ0 cryptococcu
22	39	75.0	173	2 Q5KN21_CRYNE	Q5KN21 cryptococcu
23	39	75.0	386	2 Q90XX8_ONCMY	Q90XX8 oncorhynch
24	39	75.0	388	2 Q90XX7_ONCMY	Q90XX7 oncorhynch
25	39	75.0	392	2 Q91030_CHICK	Q91030 gallus gall
26	39	75.0	414	2 Q918A1_CHICK	Q918A1 gallus gall
27	39	75.0	417	2 Q90XX6_ONCMY	Q90XX6 oncorhynch
28	39	75.0	417	2 Q918A0_CHICK	Q918A0 gallus gall
29	39	75.0	432	2 Q9XUJ4_CAEFL	Q9XUJ4 caenorhabdi
30	39	75.0	518	2 Q4WT51_ASPFU	Q4WT51 aspergillus
31	39	75.0	556	2 Q80HR4_9CLOS	Q80HR4 strawberry

32	39	75.0	556	2 Q805J2_9CLOS	Q805j2 strawberry
33	39	75.0	827	2 Q7Z1Z0_DROME	Q7z1z0 drosophila
34	39	75.0	832	2 Q7KUZ9_DROME	Q7kuz9 drosophila
35	38	73.1	391	2 Q4RP32_TETNG	Q4rp32 tetraodon n
36	38	73.1	404	1 GATA5_MOUSE	P97489 mus musculu
37	38	73.1	404	2 Q961J8_HUMAN	Q961j8 homo sapien
38	38	73.1	404	2 Q5U2V0_RAT	Q5u2v0 rattus norv
39	38	73.1	425	1 EXG_CANOL	Q8nkf9 candida ole
40	38	73.1	559	2 Q753Z9_ASHGO	Q753z7 treponema p
41	38	73.1	577	1 PYRG_TREPA	O83327 treponema p
42	38	73.1	3930	2 Q54HJ6_DICDI	Q54hj6 dictyosteli
43	37	71.2	87	2 Q7MJZ0_VIBVY	Q7mjz0 vibrio vuln
44	37	71.2	113	2 Q8YUX6_ANASP	Q8yux6 anabaena sp
45	37	71.2	188	2 Q14901_HUMAN	Q14901 homo sapien

ALIGNMENTS

RESULT 1
Q6P138_HUMAN
ID Q6P138_HUMAN PRELIMINARY; PRT; 249 AA.
AC Q6P138;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WT1 protein.
GN Name=WT1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RX NIH MGC Project;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC046461; AAH46461.1; -, mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms_tumour.
DR Pfam; PF02165; WT1.1
DR PRINTS; PR00049; WILMSTUMOUR.
DR SEQUENCE 249 AA; 25967 MW; 33F53B96A79CBF28 CRC64;
SQ
Query Match 100.0%; Score 52; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPYLPSCL 9

Db 130 NAPYLPSCL 138

RESULT 2

Q4VXV5 HUMAN
Q4VXV5_HUMAN PRELIMINARY; PRT; 429 AA.
AC Q4VXV5_HUMAN PRELIMINARY; PRT; 429 AA.
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE WILMS tumour 1.
GN Name=Wt1; ORFNames=AL049692.1-001;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Frankland J.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

RL EMBL; AL049692; CAI95759.1; -; Genomic_DNA.

DR InterPro; IPR000976; WILMS tumour.

DR InterPro; IPR007087; Znf_C2H2.

DR Pfam; PF02165; Wt1; 1.

DR Pfam; PF00096; Zf-C2H2; 4.

DR PRINTS; PR00049; WILMSTUMOUR.

DR ProDom; PD000003; Znf_C2H2; 2.

DR SMART; SM00355; Znf_C2H2; 4.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.

DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.

DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.

DR Metal-binding; Nuclear protein; Zinc; Zinc-finger.

KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.

SQ SEQUENCE 429 AA; 47195 MW; C2F9912E0A4DA3DB CRC64;

Query Match 100.0%; Score 52; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPYLPSCL 9

Db 130 NAPYLPSCL 138

RESULT 3

Q4VXV6 HUMAN
Q4VXV6_HUMAN PRELIMINARY; PRT; 432 AA.
AC Q4VXV6;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE WILMS tumor 1.
GN Name=Wt1; ORFNames=AL049692.1-003;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Frankland J.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

RL EMBL; AL049692; CAI95758.1; -; Genomic_DNA.

DR InterPro; IPR000976; WILMS tumour.

DR InterPro; IPR007087; Znf_C2H2.

DR Pfam; PF02165; Wt1; 1.

DR Pfam; PF00096; Zf-C2H2; 4.

DR PRINTS; PR00049; WILMSTUMOUR.

DR ProDom; PD000003; Znf_C2H2; 2.

DR SMART; SM00355; Znf_C2H2; 4.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 432 AA; 47511 MW; 1ACA6CE3563DA9D2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPYLPSCL 9

Db 130 NAPYLPSCL 138

RESULT 4

WT1_RAT
WT1_RAT STANDARD; PRT; 448 AA.
AC P49552;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Wt1; tumor protein, homolog.
GN Name=Wt1; Synonyms=Wt-1;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4).
RX STRAIN=Sprague-Dawley; ISSUES=Kidney;
RX MEDLINE=93046155; PubMed=1330293;
RA Sharma P.M., Yang X., Bowman M., Roberts V., Sukumar S.;
RT "Molecular cloning of rat Wt1s, tumor complementary DNA and a study
of messenger RNA expression in the urogenital system and the brain."
Cancer Res. 52:6407-6412(1992).
CC -!- FUNCTION: Potential role in transcriptional regulation. Recognizes
and binds to the DNA sequence 5'-CGCCCCCGC-3'.
CC -!- SUBUNIT: Interacts with ZNF224 via the zinc-finger region.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=P49952-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P49952-2; Sequence=VSP_006872, VSP_006873;
CC Name=3;
CC IsoId=P49952-3; Sequence=VSP_006872;
CC Name=4;
CC IsoId=P49952-4; Sequence=VSP_006873;
CC -!- TISSUE SPECIFICITY: Kidney.
CC -!- DEVELOPMENTAL STAGE: Expressed during kidney development.
CC -!- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein
family.
CC -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.

This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; X69716; CAA49373.1; -; mRNA.

HSSP; P08046; 1F21.

TRANSFAC; T02352; -.

Ensembl; ENSRNOG0000013074; Rattus norvegicus.

RGD; 3974; Wt1.

InterPro; IPR000976; Wt1s tumour.

InterPro; IPR007087; Znf_C2H2.

Pfam; PF02165; Wt1; 1.

Pfam; PF00096; Zf-C2H2; 4.

PRINTS; PR00049; WILMSTUMOUR.

DR Prodom; PD000003; Znf C2H2; 2.
DR SMART; SM00355; Znf C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
KW Alternative splicing; Anti-oncogene; Cell cycle; DNA-binding;
KW Metal-binding; Nuclear protein; Repeat; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 322 346 C2H2-type 1.
FT ZN_FING 352 376 C2H2-type 2.
FT ZN_FING 382 404 C2H2-type 3.
FT ZN_FING 413 437 C2H2-type 4.
FT COMPBIAS 27 82 Pro-rich.
FT VARSPLIC 249 265 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 407 409 /FTId=VSP 006872.
FT VARSPLIC 407 409 Missing (in isoform 2 and isoform 4).
FT VARSPLIC 407 409 /FTId=VSP 006873.
SQ SEQUENCE 448 AA; 49193 MW; 329AC9AC1FF73F76 CRC64;
Query Match 100.0%; Score 52; DB 1; Length 448;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NAPYLPSC 9
Db 129 NAPYLPSC 137
RESULT 5
WT1_HUMAN STANDARD; PRT; 449 AA.
ID P19544; Q15981; Q16256; Q16575; Q81Y25;
AC P19544; Q15981; Q16256; Q16575; Q81Y25;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Wilms' tumor protein (WT33).
GN Name=WT1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal kidney;
RX MEDLINE=90158822; PubMed=2154702; DOI=10.1038/343774a0;
RA Gessler M., Poustka A., Cavenee W., Neve R.L., Orkin S.H.,
RB Bruns G.A.P.;
RT "Homozygous deletion in Wilms tumours of a zinc-finger gene identified
RT by chromosome jumping.";
RL Nature 343:774-778 (1990).
[2]
RN NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
RC TISSUE=Placenta;
RX MEDLINE=92052142; PubMed=1658787;
RA Haber D.A., Sohn R.L., Buckler A.J., Pelletier J., Call K.M.,
RB Housman D.E.;
RT "Alternative splicing and genomic structure of the Wilms tumor gene
RT WT1.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9618-9622 (1991).
[3]
RN NUCLEOTIDE SEQUENCE (ISOFORM 4).
RX MEDLINE=92241883; PubMed=1572653;
RA Gessler M., Konig A., Bruns G.A.P.;
RT "The genomic organization and expression of the WT1 gene.";
RL Genomics 12:807-813 (1992).
[4]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIHGS-SNPs, environmental genome project, NIHGS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

RN NUCLEOTIDE SEQUENCE OF 85-449.
RP MEDLINE=90150277; PubMed=2154335; DOI=10.1016/0092-8674(90)90601-A;
RX Call K.M., Glaser T., Ito C.Y., Buckler A.J., Pelletier J., C.,
RA Haber D.A., Rose E.A., Kral A., Yeager H., Lewis W.H., Jones C.,
RB Housman D.E.;
RT "Isolation and characterization of a zinc finger polypeptide gene at
RT the human chromosome 11 Wilms' tumor locus.";
RL Cell 60:509-520 (1990).
[6]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP Human chromosome 11 international sequencing consortium;
RG Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[7]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 148-449 (ISOFORM 4).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Maman A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[8]
RN NUCLEOTIDE SEQUENCE OF 301-449.
RP TISSUE=Fetal kidney;
RC MEDLINE=95166649; PubMed=7862533;
RX Hamilton T.B., Barilla K.C., Romaniuk P.J.;
RA "High affinity binding sites for the Wilms' tumour suppressor protein
RT WT1.";
RL Nucleic Acids Res. 23:277-284 (1995).
[9]
RN IDENTIFICATION OF START CODON, AND ALTERNATIVE SPLICE SITES.
RX MEDLINE=91141522; PubMed=1671709;
RA Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.;
RT "Isolation, characterization, and expression of the murine Wilms'
RT tumor gene (WT1) during kidney development.";
RL Mol. Cell. Biol. 11:1707-1712 (1991).
[10]
RN INTERACTION WITH WTAP.
RP MEDLINE=20458888; PubMed=11001926;
RX Little N.A., Hastie N.D., Davies R.C.;
RT "Identification of WTAP, a novel Wilms' tumour 1-associating
RT protein.";
RL Hum. Mol. Genet. 9:2231-2239 (2000).
[11]
RN INTERACTION WITH ZNF224.
RP PubMed=12239212; DOI=10.1074/jbc.M205667200;
RX Lee T.H., Lwu S., Kim J., Pelletier J.;
RT "Inhibition of Wilms tumor 1 transactivation by bone marrow zinc
RT finger 2, a novel transcriptional repressor.";
RL J. Biol. Chem. 277:44826-44837 (2002).
[12]
RN REVIEW.
RP MEDLINE=92207913; PubMed=1313285;
RX Haber D.A., Buckler A.J.;
RT "WT1: a novel tumor suppressor gene inactivated in Wilms' tumor.";
RL New Biol. 4:97-106 (1992).
[13]


```
DR GO:0005737; C:cytoplasm; IDA.
DR GO:0005634; C:nucleus; IDA.
DR GO:0005515; F:protein binding; IPI.
DR GO:0030855; F:epithelial cell differentiation; IMP.
DR GO:0001747; P:eye morphogenesis (sensu Mammalia); IMP.
DR GO:0001728; P:germ cell development; IMP.
DR GO:0008886; P:histogenesis; IMP.
DR GO:0008584; P:male gonad development; IMP.
DR GO:0001823; P:mesonephros development; IMP.
DR GO:0001656; P:metanephros development; IMP.
DR GO:0006357; P:regulation of transcription from RNA polyme. . .; IDA.
DR InterPro: IPR000976; Wilms tumour.
DR InterPro: IPR007087; Wilms tumour.
DR Pfam: PF02165; WT1; 1.
DR Pfam: PF00096; zf-C2H2; 4.
DR PRINTS: PR00049; WILMSTUMOUR.
DR ProDom: PD000003; Znf C2H2; 2.
DR SMART: SM00355; Znf C2H2; 4.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 4.
KW Alternative splicing; Anti-oncogene; Cell cycle; DNA-binding;
KW Metal-binding; Nuclear protein; Repeat; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 323 347 C2H2-type 1.
FT ZN_FING 353 377 C2H2-type 2.
FT ZN_FING 383 405 C2H2-type 3.
FT ZN_FING 414 438 C2H2-type 4.
FT COMBIAS 28 83 Pro-rich.
FT VARSP LIC 250 266 Missing (in isoform 2 and isoform 3).
FT VARSP LIC 408 410 Missing (in isoform 2 and isoform 4).
FT VARSP LIC 408 410 /FTID=VSP_006869.
FT SEQUENCE 449 AA; 49246 MW; 962381E9C8D7A380 CRC64;
Query Match 100.0%; Score 52; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NAYPLPSC L 9
DB 130 NAYPLPSC L 138
RESULT 7
WT1_PIG STANDARD; PRT; 449 AA.
AC O6251;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Wilms' tumor protein homolog.
GN Name=WT1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OC NCBI_TaxID=9823;
-RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4).
RC STRAIN=LMD; TISSUE=Kidney;
RA MEDLINE=98267201; PubMed=9602131; DOI=10.1016/S0378-1119(98)00112-7;
RA Teurttani N., Oda H., Nakatsuru Y., Imai Y., Zhang S., Ueno Y.,
RA Ishikawa T.;
RT "cDNA cloning and developmental expression of the porcine homologue of
RT WT1."
RL Gene 211.215-220(1998).
CC -!- FUNCTION: Potential role in transcriptional regulation. Recognizes
CC and binds to the DNA sequence 5'-CGCCCCCG-3'.
CC -!- SUBUNIT: Interacts with ZNF224 via the zinc-finger region.
CC Interacts with WTAP (by similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
```

```
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1; Sequence=Displayed;
CC Name=2; Sequence=VSP_006870, VSP_006871;
CC Name=3; Sequence=VSP_006870;
CC Name=4; Sequence=VSP_006871;
CC -!- DEVELOPMENTAL STAGE: Expressed during kidney development.
CC -!- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein
CC family.
CC -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AB010969; BAA28147.1; -; mRNA.
CC HSP; P08046; 1F21.
CC InterPro: IPR000976; Wilms tumour.
CC InterPro: IPR007087; Znf C2H2.
CC Pfam: PF02165; WT1; 1.
CC Pfam: PF00096; zf-C2H2; 4.
CC PRINTS: PR00049; WILMSTUMOUR.
CC ProDom: PD000003; Znf C2H2; 2.
CC SMART: SM00355; Znf C2H2; 4.
CC PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
CC PROSITE: PS0157; ZINC_FINGER_C2H2_2; 4.
KW Alternative splicing; Anti-oncogene; Cell cycle; DNA-binding;
KW Metal-binding; Nuclear protein; Repeat; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 323 347 C2H2-type 1.
FT ZN_FING 353 377 C2H2-type 2.
FT ZN_FING 383 405 C2H2-type 3.
FT ZN_FING 414 438 C2H2-type 4.
FT COMBIAS 28 83 Pro-rich.
FT VARSP LIC 249 265 Missing (in isoform 2 and isoform 3).
FT VARSP LIC 407 409 Missing (in isoform 2 and isoform 4).
FT VARSP LIC 407 409 /FTID=VSP_006871.
FT SEQUENCE 449 AA; 49166 MW; 9C3E557B96F5A7B3 CRC64;
Query Match 100.0%; Score 52; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NAYPLPSC L 9
DB 130 NAYPLPSC L 138
RESULT 8
O42223_TRASC PRELIMINARY; PRT; 390 AA.
AC O42223;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wilms tumor 1 protein.
GN Name=WT1;
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
OC NCBI_TaxID=34903;
-RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Spottila L.D., Hall S.E.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF019779; AAB70832.1; -; mRNA.
```

```
DR HSP; P08046; 1P47.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wfms tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; Wt1; 1.
DR Pfam; PF00096; zf-C2H2; 3.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 390 AA; 43620 MW; 1C9987435BE927C2 CRC64;

Query Match 86.5%; Score 45; DB 2; Length 390;
Best Local Similarity 77.8%; Pred No. 7; 1; Mismatches 1; Indels 1; Gaps 0;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 NAPPYPSCL 9
Db 113 NGPYLPNCL 121

RESULT 9
Q5W611_CYNPY
ID Q5W611_CYNPY PRELIMINARY; PRT; 426 AA.
AC Q5W611;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wt1.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=99081568; PubMed=9865970;
RX DOI=10.1046/j.1440-169X.1998.t01-4-00004.x;
RA Nakayama Y., Yamamoto T., Matsuda Y., Abe S.-I.;
RT "Cloning of cDNA for newt Wt1 and the differential expression during
RT spermatogenesis of the Japanese newt, Cynops pyrrhogaster.";
RL Dev. Growth Differ. 40:599-608(1998).
DR EMBL; AB013886; BAA76399.1; -; mRNA.
DR HSP; P08046; 1P47.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wfms tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; Wt1; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 426 AA; 47591 MW; 46A0B158A9F79C6C CRC64;

Query Match 86.5%; Score 45; DB 2; Length 426;
Best Local Similarity 77.8%; Pred No. 7; 8;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
```

```
Qy 1 NAPPYPSCL 9
Db 120 NGPYLPNCL 128

RESULT 10
P87542_9CLOS
ID P87542_9CLOS PRELIMINARY; PRT; 225 AA.
AC P87542;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HSP 70 homolog (Fragment).
OS Beet pseudo-Yellows virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Crinivirus.
OX NCBI_TaxID=72750;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-California;
RC Tian T., Klaassen V.A., Soong J., Wisler G., Duffus J.E., Falk B.W.;
RT "Generation of cDNAs specific to lettuce infectious yellows
RT closterovirus and other whitefly-transmitted viruses by using RT-PCR
RT and degenerate oligonucleotide primers corresponding to the
RT closterovirus gene encoding the heat shock protein 70 homolog.";
RL Phytopathology 0:0-0(1996).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; U67447; AAB40655.1; -; Genomic_RNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR ProDom; PD000083; Hsp70; 1.
DR PROSITE; PS00323; HSP70_2; UNKNOWN_1.
KW ATP-binding; Nucleotide-binding.
FT NON-TER 1
FT NON-TER 225
SQ SEQUENCE 225 AA; 24967 MW; 0D150BD4143AAD3 CRC64;

Query Match 84.6%; Score 44; DB 2; Length 225;
Best Local Similarity 66.7%; Pred. No. 6; 1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPPYPSCL 9
Db 26 NSPYIPTCL 34

RESULT 11
Q80625_9CLOS
ID Q80625_9CLOS PRELIMINARY; PRT; 554 AA.
AC Q80625;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
GN Name=Hsp70;
OS Cucumber yellows virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Crinivirus.
OX NCBI_TaxID=32618;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541874; PubMed=12655104; DOI=10.1099/vir.0.18605-0;
RX Hartono S., Natsuaki T., Genda Y., Okuda S.;
RT "Nucleotide sequence and genome organization of Cucumber yellows
RT virus, a member of the genus Crinivirus.";
RL J. Gen. Virol. 84:1007-1012(2003).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB085612; BAC6364.1; -; Genomic_RNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
```

```
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; HSP70; 1.
DR PROSITE; PS00329; HSP70_2; UNKNOWN_1.
KW ATP-binding; Heat shock; Nucleotide-binding.
SQ SEQUENCE 554 AA; 61810 MW; 178FCAC640C7313C CRC64;

Query Match      84.6%; Score 44; DB 2; Length 554;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSC 9
DB 31 NSPYIPTCL 39

RESULT 12
ID Q6VRA5_9CLOS PRELIMINARY; PRT; 554 AA.
AC Q6VRA5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE HSP70h.
OS Beet pseudo-yellow virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Crinivirus.
OX NCBI_TaxID=72750;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tzanetakis I.E., Wintermantel W.M., Martin R.R.;
RT "First report of Beet pseudoyellows virus in strawberry in the USA: A
RT second crinivirus able to cause pallidosis disease.";
RL Plant Dis. 87:1398-1398(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tzanetakis I.E., Martin R.R.;
RT "First Report of Beet pseudo yellows virus in Blackberry in the United
RT States.";
RL Plant Dis. 88:223-223(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15266105; DOI=10.1023/B:VIRU.0000025771.48128.f8;
RA Tzanetakis I.E., Martin R.R.;
RT "Complete nucleotide sequence of a strawberry isolate of Beet
RT pseudoyellows virus.";
RL Virus Genes 28:239-246(2004).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY330919; AAQ97386.1; -; Genomic_RNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; HSP70; 1.
DR PROSITE; PS00329; HSP70_2; UNKNOWN_1.
KW ATP-binding; Nucleotide-binding.
SQ SEQUENCE 554 AA; 61677 MW; BB7F061DE1D010C8 CRC64;

Query Match      84.6%; Score 44; DB 2; Length 554;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSC 9
DB 31 NSPYIPTCL 39

RESULT 13
Q5ICV4_9CLOS
ID Q5ICV4_9CLOS PRELIMINARY; PRT; 555 AA.
AC Q5ICV4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
```

```
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE P62.
OS Blackberry yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Crinivirus.
OX NCBI_TaxID=265878;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15664053; DOI=10.1016/j.jviromet.2004.11.006;
RA Tzanetakis I.E., Keller K.E., Martin R.R.;
RT "The use of reverse transcriptase for efficient first- and second-
RT strand cDNA synthesis from single- and double-stranded RNA
RT templates.";
RL J. Virol. Methods 124:73-77(2005).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY776335; AAV40966.1; -; Genomic_RNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; HSP70; 1.
DR PROSITE; PS00329; HSP70_2; UNKNOWN_1.
KW ATP-binding; Nucleotide-binding.
SQ SEQUENCE 555 AA; 62138 MW; 618A8158FBE2B6F6 CRC64;

Query Match      84.6%; Score 44; DB 2; Length 555;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPYLPSC 9
DB 32 NSPYIPTCL 40

RESULT 14
Q5FYX8_9CLOS
ID Q5FYX8_9CLOS PRELIMINARY; PRT; 555 AA.
AC Q5FYX8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE P62.
OS Blackberry yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Crinivirus.
OX NCBI_TaxID=265878;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Navaho-HCRL;
RA Tzanetakis I.E., Susaimuthu J., Gergerich R.C., Martin R.R.;
RT "Characterization of Blackberry yellow vein virus.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY873920; AAW67738.1; -; Genomic_RNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; HSP70; 1.
DR PROSITE; PS00329; HSP70_2; UNKNOWN_1.
KW ATP-binding; Nucleotide-binding.
SQ SEQUENCE 555 AA; 62162 MW; FE2A25461063C1B9 CRC64;

Query Match      84.6%; Score 44; DB 2; Length 555;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NPYLPSC 9
DB 32 NSPYIPTCL 40

RESULT 15
```

```

Q5FYV1_9CLOS
ID Q5FYV1_9CLOS PRELIMINARY; PRT; 555 AA.
AC Q5FYV1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE P62.
OS Blackberry yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC Crinivirus.
OX NCBI_TaxID=265878;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Chickasaw-Arkansas B, and Chickasaw-Arkansas A;
RA Tzanetakis I E, Susaimuthu J, Gergerich R C, Martin R R.;
RT "Characterization of Blackberry yellow vein virus ";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY873919; AAW67735.1; -; Genomic_RNA.
DR EMBL; AY873919; AAW67734.1; -; Genomic_RNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; HSP70; 1.
DR PROSITE; PS00329; HSP70_2; UNKNOWN_1.
KW ATP-binding; Nucleotide-binding.
SQ SEQUENCE 555 AA; 62254 MW; 9453187EFD19F324 CRC64;

Query Match      84.6%; Score 44; DB 2; Length 555;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCCL 9
   |:|:|:|
DB 32 NSPYIPTCL 40

```

Search completed: May 5, 2006, 16:23:07
Job time : 232 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 16:23:21 ; Search time 47 Seconds
(without alignments)
15.832 Million cell updates/sec

Title: US-09-684-361C-144

Perfect score: 52
Sequence: 1 NAPYLPSCCL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
 - 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
 - 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
 - 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
 - 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
 - 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	154	1	US-08-102-942A-5
2	52	100.0	154	2	US-09-037-179B-5
3	52	100.0	154	2	US-09-929-315-5
4	52	100.0	210	1	US-08-234-783-2
5	52	100.0	210	1	US-08-456-907-2
6	52	100.0	210	4	PCT-US95-05523-2
7	52	100.0	345	1	US-08-102-942A-2
8	52	100.0	345	2	US-09-037-179B-2
9	52	100.0	345	2	US-09-929-315-2
10	52	100.0	429	1	US-08-234-783-4
11	52	100.0	429	1	US-08-456-907-4
12	52	100.0	429	4	PCT-US95-05523-4
13	52	100.0	449	1	US-08-102-942A-4
14	52	100.0	449	1	US-08-102-942A-6
15	52	100.0	449	2	US-09-037-179B-4
16	52	100.0	449	2	US-09-037-179B-6
17	52	100.0	449	2	US-09-538-092-960
18	52	100.0	449	2	US-09-929-315-4
19	52	100.0	449	2	US-09-929-315-6
20	52	100.0	559	2	US-09-949-016-9138
21	52	100.0	559	2	US-09-949-016-9139
22	52	100.0	559	2	US-09-949-016-9140
23	52	100.0	559	2	US-09-949-016-9141
24	52	100.0	576	2	US-09-949-016-9404
25	52	100.0	576	2	US-09-949-016-9405
26	52	100.0	576	2	US-09-949-016-9406
27	52	100.0	576	2	US-09-949-016-9407

28	37	71.2	431	2	US-09-248-796A-17264	Sequence 17264, A
29	36	69.2	209	2	US-09-107-532A-3667	Sequence 3667, Ap
30	36	69.2	218	2	US-09-134-000C-4932	Sequence 4932, Ap
31	36	69.2	220	2	US-09-134-000C-5305	Sequence 5305, Ap
32	36	69.2	513	2	US-09-949-016-5993	Sequence 5993, Ap
33	36	69.2	536	2	US-09-949-016-10134	Sequence 10134, A
34	36	69.2	594	2	US-09-650-324A-59	Sequence 59, Appl
35	36	69.2	594	2	US-10-039-112A-59	Sequence 59, Appl
36	35	67.3	200	2	US-09-328-352-7282	Sequence 7282, Ap
37	35	67.3	207	2	US-09-893-737-160	Sequence 160, App
38	35	67.3	209	2	US-09-583-110-4034	Sequence 4034, Ap
39	35	67.3	212	2	US-09-107-433-4692	Sequence 4692, Ap
40	35	67.3	280	2	US-09-538-092-558	Sequence 558, App
41	35	67.3	730	1	US-08-121-713D-58	Sequence 58, Appl
42	35	67.3	730	1	US-08-835-268-58	Sequence 58, Appl
43	35	67.3	730	1	US-09-060-692-58	Sequence 58, Appl
44	35	67.3	730	2	US-08-833-391-58	Sequence 58, Appl
45	35	67.3	730	2	US-09-060-610-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-08-102-942A-5
; Sequence 5, Application US/08102942A
; Patent No. 5726288
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,942A
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5194A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-102-942A-5

```
Query Match      100.0%; Score 52; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 NAYPLPSCL 9
Db 44 NAYPLPSCL 52

RESULT 2
US-09-037-179B-5
; Sequence 5, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR FILING DATE: 1990-11-13
; PRIOR FILING DATE: 1989-11-13
; PRIOR FILING DATE: 1989-11-13
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-037-179B-5

Query Match      100.0%; Score 52; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 NAYPLPSCL 9
Db 44 NAYPLPSCL 52

RESULT 3
US-09-929-315-5
; Sequence 5, Application US/09929315
; Patent No. 6943011
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; FILE REFERENCE: 0050.1312-013
; CURRENT APPLICATION NUMBER: US/09/929,315

Query Match      100.0%; Score 52; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 NAYPLPSCL 9
Db 44 NAYPLPSCL 52

RESULT 4
US-08-234-783-2
; Sequence 2, Application US/08234783
; Patent No. 5622835
; GENERAL INFORMATION:
; APPLICANT: Herlyn, Meenhard
; APPLICANT: Morris, Jennifer
; APPLICANT: Rauscher III, Frank J.
; APPLICANT: Rodeck, Ulrich
; TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of
; TITLE OF INVENTION: Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,783
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-234-783-2

Query Match      100.0%; Score 52; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.17;
```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSC1 9

Db 141 NAPYLPSC1 149

RESULT 5

US-08-456-907-2
; Sequence 2, Application US/08456907
; Patent No. 5633142
; GENERAL INFORMATION:
; APPLICANT: Herlyn, Meenhard
; APPLICANT: Morris, Jennifer
; APPLICANT: Rauscher III, Frank J.
; APPLICANT: Rodeck, Ulrich
; TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of
; TITLE OF INVENTION: Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,907
; FILING DATE:
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,783
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-456-907-2
Query Match 100.0%; Score 52; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NAPYLPSC1 9
Db 141 NAPYLPSC1 149

RESULT 6

PCT-US95-05523-2
; Sequence 2, Application PC/TUS9505523
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; TITLE OF INVENTION: Wt1 Monoclonal Antibodies and
; TITLE OF INVENTION: Methods of Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457

CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05523
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,783
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST48PCT
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US95-05523-2
Query Match 100.0%; Score 52; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NAPYLPSC1 9
Db 141 NAPYLPSC1 149

RESULT 7

US-08-102-942A-2
; Sequence 2, Application US/08102942A
; Patent No. 5726288
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David B.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,942A
; FILING DATE: 02-AUG-1993

```
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5194A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-102-942A-2

Query Match      100.0%; Score 52; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NAYLPSCSL 9
DB      46 NAYLPSCSL 54

RESULT 8
US-09-037-179B-2
; Sequence 2, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR FILING DATE: 1990-11-13
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-037-179B-2

Query Match      100.0%; Score 52; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NAYLPSCSL 9
DB      46 NAYLPSCSL 54

RESULT 9
US-09-929-315-2
; Sequence 2, Application US/09929315
```

```
; Patent No. 6943011
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; FILE REFERENCE: 0050.1312-013
; CURRENT APPLICATION NUMBER: US/09/929,315
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 09/037,179
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1991-11-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-929-315-2

Query Match      100.0%; Score 52; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NAYLPSCSL 9
DB      46 NAYLPSCSL 54

RESULT 10
US-08-234-783-4
; Sequence 4, Application US/08234783
; Patent No. 5622835
; GENERAL INFORMATION:
; APPLICANT: Herlyn, Meenhard
; APPLICANT: Morris, Jennifer
; APPLICANT: Rauscher III, Frank J.
; APPLICANT: Rodack, Ulrich
; TITLE OF INVENTION: Wtl Monoclonal Antibodies and Methods of
; TITLE OF INVENTION: Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,783
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```



```

; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-234-783-4
;
Query Match 100.0%; Score 52; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAYLPSCSL 9
Db 130 NAYLPSCSL 138

RESULT 11
US-08-456-907-4
; Sequence 4, Application US/08456907
; Patent No. 5633142
; GENERAL INFORMATION:
; APPLICANT: Herlyn, Meenhard
; APPLICANT: Morris, Jennifer
; APPLICANT: Rauscher III, Frank J.
; APPLICANT: Rodeck, Ulrich
; TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of
; TITLE OF INVENTION: Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,907
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,783
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-907-4
;
Query Match 100.0%; Score 52; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAYLPSCSL 9
Db 130 NAYLPSCSL 138

RESULT 12
PCT-US95-05523-4
; Sequence 4, Application PC/TUS9505523
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; TITLE OF INVENTION: Wt1 Monoclonal Antibodies and
; TITLE OF INVENTION: Methods of Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,783
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-05523-4
;
Query Match 100.0%; Score 52; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAYLPSCSL 9
Db 130 NAYLPSCSL 138

RESULT 13
US-08-102-942A-4
; Sequence 4, Application US/08102942A
; Patent No. 5726288
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
```

```
;
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/102,942A
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5194A2
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-102-942A-4

Query Match 100.0%; Score 52; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAYLPSCSCL 9
Db 130 NAYLPSCSCL 138

RESULT 14
US-08-102-942A-6
; Sequence 6, Application US/08102942A
; Patent No. 5726288
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,942A
```

```
;
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5194A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-102-942A-6

Query Match 100.0%; Score 52; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAYLPSCSCL 9
Db 130 NAYLPSCSCL 138

RESULT 15
US-09-037-179B-4
; Sequence 4, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; CURRENT FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 449
; TYPE: amino acid
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine
; US-09-037-179B-4

Query Match 100.0%; Score 52; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAYLPSCSCL 9
Db 130 NAYLPSCSCL 138
```

Search completed: May 5, 2006, 16:24:42
Job time : 48 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 16:34:36 ; Search time 164 Seconds
(without alignments)
22.930 Million cell updates/sec

Title: US-09-684-361C-144
Perfect score: 52
Sequence: 1 NAPYLPSCSL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	3	US-09-938-864-144
2	52	100.0	9	3	US-09-938-864-282
3	52	100.0	9	3	US-09-791-477-144
4	52	100.0	9	3	US-09-791-477-282
5	52	100.0	9	3	US-09-785-019-144
6	52	100.0	9	3	US-09-785-019-282
7	52	100.0	9	4	US-10-125-635A-144
8	52	100.0	9	4	US-10-125-635A-282
9	52	100.0	9	4	US-10-002-603-144
10	52	100.0	9	4	US-10-002-603-282
11	52	100.0	9	4	US-10-195-835-144
12	52	100.0	9	4	US-10-195-835-282
13	52	100.0	9	4	US-10-286-333-144
14	52	100.0	9	4	US-10-286-333-282
15	52	100.0	9	4	US-10-244-830-144
16	52	100.0	9	4	US-10-244-830-282
17	52	100.0	9	4	US-10-427-717-144
18	52	100.0	9	4	US-10-427-717-282
19	52	100.0	9	4	US-10-648-780-144
20	52	100.0	9	4	US-10-648-780-282
21	52	100.0	23	3	US-09-938-864-2
22	52	100.0	23	3	US-09-938-864-3
23	52	100.0	23	3	US-09-791-477-2
24	52	100.0	23	3	US-09-791-477-3
25	52	100.0	23	3	US-09-785-019-2
26	52	100.0	23	3	US-09-785-019-3
27	52	100.0	23	4	US-10-125-635A-2

28	52	100.0	23	4	US-10-125-635A-3
29	52	100.0	23	4	US-10-002-603-2
30	52	100.0	23	4	US-10-002-603-3
31	52	100.0	23	4	US-10-195-835-2
32	52	100.0	23	4	US-10-195-835-3
33	52	100.0	23	4	US-10-286-333-2
34	52	100.0	23	4	US-10-286-333-3
35	52	100.0	23	4	US-10-244-830-2
36	52	100.0	23	4	US-10-244-830-3
37	52	100.0	23	4	US-10-427-717-2
38	52	100.0	23	4	US-10-427-717-3
39	52	100.0	23	4	US-10-648-780-2
40	52	100.0	23	4	US-10-648-780-3
41	52	100.0	152	3	US-09-938-864-343
42	52	100.0	152	3	US-09-785-019-343
43	52	100.0	152	4	US-10-125-635A-343
44	52	100.0	152	4	US-10-002-603-343
45	52	100.0	152	4	US-10-195-835-343

ALIGNMENTS

RESULT 1
US-09-938-864-144
; Sequence 144, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-144

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPYLPSCSL 9
Db 1 NAPYLPSCSL 9

RESULT 2
US-09-938-864-282
; Sequence 282, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence

```
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-282

Query Match      100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NAPYLPSCl 9
Db      1 NAPYLPSCl 9

RESULT 3
US-09-791-477-144
; Sequence 144, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-144

Query Match      100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NAPYLPSCl 9
Db      1 NAPYLPSCl 9

RESULT 4
US-09-791-477-282
; Sequence 282, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-282

Query Match      100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NAPYLPSCl 9
Db      1 NAPYLPSCl 9

RESULT 5
US-09-785-019-144
; Sequence 144, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-144

Query Match      100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 NAPYLPSCl 9
Db      1 NAPYLPSCl 9

RESULT 6
US-09-785-019-282
; Sequence 282, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-785-019-282

Query Match      100.0%; Score 52; DB 3; Length 9;
```

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 NAYLPSCSCL 9
| | | | | | | | | |
Db 1 NAYLPSCSCL 9

RESULT 7
US-10-125-635A-144
; Sequence 144, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-125-635A-144

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAYLPSCSCL 9
| | | | | | | | | |
Db 1 NAYLPSCSCL 9

RESULT 8
US-10-125-635A-282
; Sequence 282, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-125-635A-282

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAYLPSCSCL 9
| | | | | | | | | |
Db 1 NAYLPSCSCL 9

RESULT 9
US-10-002-603-144
; Sequence 144, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-002-603-144

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAYLPSCSCL 9
| | | | | | | | | |
Db 1 NAYLPSCSCL 9

RESULT 10
US-10-002-603-282
; Sequence 282, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-002-603-282

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAYLPSCSCL 9
| | | | | | | | | |
Db 1 NAYLPSCSCL 9

```

RESULT 11
US-10-195-835-144
; Sequence 144, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Derrick A.
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195,835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-195-835-144

Query Match          100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCl 9
DB 1 NAPYLPSCl 9

RESULT 12
US-10-195-835-282
; Sequence 282, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Derrick A.
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Mossman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195,835
; CURRENT FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-195-835-282

Query Match          100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCl 9
DB 1 NAPYLPSCl 9

RESULT 13
US-10-286-333-144
; Sequence 144, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Java, No. US20030215458A1a1ie
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-286-333-144

Query Match          100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCl 9
DB 1 NAPYLPSCl 9

RESULT 14
US-10-286-333-282
; Sequence 282, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Java, No. US20030215458A1a1ie
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 282
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-286-333-282

Query Match          100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSCl 9
DB 1 NAPYLPSCl 9

RESULT 15
US-10-244-830-144
; Sequence 144, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; CURRENT FILING DATE: 2002-09-16

```



```
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-244-830-144

Query Match      100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. NO. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NAPYLPSC 9
        |||||
Db      1 NAPYLPSC 9

Search completed: May 5, 2006, 16:38:16
Job time : 165 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 16:35:41 ; Search time 26 Seconds
(without alignments)
16.022 Million cell updates/sec

Title: US-09-684-361C-144
Perfect score: 52
Sequence: 1 NAYLPSCSL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues
Total number of hits satisfying chosen parameters: 235405
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New.*
1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep1.*
2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
7: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep1.*
8: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
9: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep1.*
10: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
11: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	280	US-11-071-062-3	Sequence 3, Appli
2	52	100.0	292	US-11-071-062-5	Sequence 5, Appli
3	52	100.0	429	US-11-071-062-9	Sequence 9, Appli
4	52	100.0	449	US-11-071-062-1	Sequence 1, Appli
5	52	100.0	449	US-11-196-459-1	Sequence 1, Appli
6	52	100.0	449	US-11-196-459-2	Sequence 2, Appli
7	52	100.0	578	US-11-222-451-8	Sequence 8, Appli
8	35	67.3	77	US-11-045-004-2250	Sequence 2250, Ap
9	35	67.3	266	US-11-096-568A-3901	Sequence 3901, Ap
10	35	67.3	348	US-11-087-099-5780	Sequence 5780, Ap
11	35	67.3	348	US-11-087-099-7924	Sequence 7924, Ap
12	35	67.3	348	US-11-188-298-7313	Sequence 7313, Ap
13	35	67.3	348	US-11-188-298-16316	Sequence 16316, A
14	35	67.3	358	US-11-087-099-12012	Sequence 12012, A
15	35	67.3	358	US-11-096-568A-3900	Sequence 3900, Ap
16	35	67.3	358	US-11-188-298-11076	Sequence 11076, A
17	35	67.3	387	US-11-096-568A-3899	Sequence 3899, Ap
18	35	67.3	2767	US-11-100-640-38	Sequence 72, Appli
19	35	67.3	2768	US-10-510-101-72	Sequence 72, Appli
20	35	67.3	3003	US-10-453-372-1080	Sequence 1080, Ap
21	35	67.3	3361	US-10-453-372-1082	Sequence 1082, Ap

22	34	65.4	690	11	US-11-087-099-2239	Sequence 2239, Ap
23	34	65.4	690	11	US-11-188-298-2182	Sequence 2182, Ap
24	34	65.4	716	11	US-11-188-298-9887	Sequence 9887, Ap
25	34	65.4	1217	11	US-11-072-512-2263	Sequence 2263, Ap
26	33	63.5	131	11	US-11-062-186-65	Sequence 65, Appli
27	33	63.5	203	11	US-11-062-186-70	Sequence 70, Appli
28	33	63.5	206	11	US-11-062-186-69	Sequence 69, Appli
29	33	63.5	208	11	US-11-062-186-63	Sequence 63, Appli
30	33	63.5	213	11	US-11-062-186-67	Sequence 67, Appli
31	33	63.5	224	11	US-11-062-186-64	Sequence 64, Appli
32	33	63.5	229	11	US-11-062-186-68	Sequence 68, Appli
33	33	63.5	247	11	US-11-062-186-62	Sequence 62, Appli
34	33	63.5	247	11	US-11-033-039-877	Sequence 877, App
35	33	63.5	252	11	US-11-062-186-66	Sequence 66, Appli
36	33	63.5	283	9	US-10-987-663-4	Sequence 4, Appli
37	33	63.5	388	9	US-10-503-590A-4	Sequence 4, Appli
38	33	63.5	388	9	US-10-503-590A-28	Sequence 28, Appli
39	33	63.5	409	9	US-10-503-590A-2	Sequence 2, Appli
40	33	63.5	446	11	US-11-112-882-68	Sequence 68, Appli
41	33	63.5	491	9	US-10-218-784-34	Sequence 34, Appli
42	33	63.5	491	9	US-10-219-061-34	Sequence 34, Appli
43	33	63.5	491	9	US-10-219-062-34	Sequence 34, Appli
44	33	63.5	491	9	US-10-219-064-34	Sequence 34, Appli
45	33	63.5	491	9	US-10-233-134-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-11-071-062-3
; Sequence 3, Application US/11071062
; Publication No. US20050260217A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Mark E.
; APPLICANT: Mozaffarian, Afsaneh
; APPLICANT: Mossman, Sally P.
; APPLICANT: Meert, Charlie D.
; TITLE OF INVENTION: CO-ENCAPSULATED WT1 POLYPEPTIDE AND IMMUNOSTIMULANT
; FILE REFERENCE: 210121.612
; CURRENT APPLICATION NUMBER: US/11/071,062
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: US 60/550,362
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 3
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-071-062-3

Query Match 100.0%; Score 52; DB 11; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NAYLPSCSL 9
Db 129 NAYLPSCSL 137

RESULT 2
US-11-071-062-5
; Sequence 5, Application US/11071062
; Publication No. US20050260217A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Mark E.
; APPLICANT: Mozaffarian, Afsaneh
; APPLICANT: Mossman, Sally P.
; APPLICANT: Meert, Charlie D.
; TITLE OF INVENTION: CO-ENCAPSULATED WT1 POLYPEPTIDE AND IMMUNOSTIMULANT
; FILE REFERENCE: 210121.612
; CURRENT APPLICATION NUMBER: US/11/071,062
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: US 60/550,362
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 3
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-071-062-3

```
; FILE REFERENCE: 210121.612
; CURRENT APPLICATION NUMBER: US/11/071,062
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: US 60/550,362
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 5
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-071-062-5

Query Match      100.0%; Score 52; DB 11; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAYLPSCSL 9
Db 141 NAYLPSCSL 149

RESULT 3
US-11-071-062-9
; Sequence 9, Application US/11071062
; Publication No. US2005026017A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Mark E.
; APPLICANT: Mozaffarian, Afsaneh
; APPLICANT: Moseman, Sally P.
; APPLICANT: Meert, Charlie D.
; TITLE OF INVENTION: CO-ENCAPSULATED WT1 POLYPEPTIDE AND IMMUNOSTIMULANT
; TITLE OF INVENTION: MICROSPHERE FORMULATIONS AND METHODS THEREOF
; FILE REFERENCE: 210121.612
; CURRENT APPLICATION NUMBER: US/11/071,062
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: US 60/550,362
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 9
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-071-062-9

Query Match      100.0%; Score 52; DB 11; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAYLPSCSL 9
Db 130 NAYLPSCSL 138

RESULT 4
US-11-071-062-1
; Sequence 1, Application US/11071062
; Publication No. US2005026017A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Mark E.
; APPLICANT: Mozaffarian, Afsaneh
; APPLICANT: Moseman, Sally P.
; APPLICANT: Meert, Charlie D.
; TITLE OF INVENTION: CO-ENCAPSULATED WT1 POLYPEPTIDE AND IMMUNOSTIMULANT
; TITLE OF INVENTION: MICROSPHERE FORMULATIONS AND METHODS THEREOF
; FILE REFERENCE: 210121.612
; CURRENT APPLICATION NUMBER: US/11/071,062
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: US 60/550,362
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Corixa Invention Disclosure Database
```

```
; SEQ ID NO 1
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-071-062-1

Query Match      100.0%; Score 52; DB 11; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAYLPSCSL 9
Db 130 NAYLPSCSL 138

RESULT 5
US-11-196-459-1
; Sequence 1, Application US/11196459
; Publication No. US20050266014A1
; GENERAL INFORMATION:
; APPLICANT: OKA, YOSHIHIRO
; APPLICANT: SUGIYAMA, HARUO
; TITLE OF INVENTION: TUMOR ANTIGEN BASED ON PRODUCTS OF THE TUMOR SUPPRESSOR
; TITLE OF INVENTION: GENE WT1
; FILE REFERENCE: 053466/0298
; CURRENT APPLICATION NUMBER: US/11/196,459
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/09/744,815
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/JP99/04130
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: JP 10-218093
; PRIOR FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-196-459-1

Query Match      100.0%; Score 52; DB 11; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAYLPSCSL 9
Db 130 NAYLPSCSL 138

RESULT 6
US-11-196-459-2
; Sequence 2, Application US/11196459
; Publication No. US20050266014A1
; GENERAL INFORMATION:
; APPLICANT: OKA, YOSHIHIRO
; APPLICANT: SUGIYAMA, HARUO
; TITLE OF INVENTION: TUMOR ANTIGEN BASED ON PRODUCTS OF THE TUMOR SUPPRESSOR
; TITLE OF INVENTION: GENE WT1
; FILE REFERENCE: 053466/0298
; CURRENT APPLICATION NUMBER: US/11/196,459
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/09/744,815
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/JP99/04130
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: JP 10-218093
; PRIOR FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-196-459-2
```

Query Match 100.0%; Score 52; DB 11; Length 449;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSC 9
Db 130 NAPYLPSC 138

RESULT 7
US-11-222-451-8
; Sequence 8, Application US/11222451
; Publication No. US20060040356A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Guderian, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Methods of Using a Mycobacterium tuberculosis Coding
; TITLE OF INVENTION: Sequence to Facilitate Stable and High Yield Expression
; FILE REFERENCE: 014058-008010US
; CURRENT APPLICATION NUMBER: US/11/222,451
; CURRENT FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: US/09/684,215
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/158,585
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Ral2-WT1 fusion
; OTHER INFORMATION: polypeptide
US-11-222-451-8

Query Match 100.0%; Score 52; DB 11; Length 578;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLPSC 9
Db 279 NAPYLPSC 287

RESULT 8
US-11-045-004-2250
; Sequence 2250, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESEN, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNICK, CHRISTOPHE
; APPLICANT: FSIH, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA

; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2250
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-2250

Query Match 67.3%; Score 35; DB 11; Length 77;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPYLP 6
Db 51 NAPYLP 56

RESULT 9
US-11-096-568A-3901
; Sequence 3901, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3901
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(266)
; OTHER INFORMATION: Ceres Seq. ID no. 13594154
US-11-096-568A-3901
Query Match 67.3%; Score 35; DB 11; Length 266;
Best Local Similarity 83.3%; Pred. No. 51;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 8
Db 248 PYVPSC 253

RESULT 10
US-11-087-099-5780
; Sequence 5780, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5780
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Glycine max
US-11-087-099-5780

Query Match 67.3%; Score 35; DB 11; Length 348;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 8
Db 338 PYVPSC 343

RESULT 11
US-11-087-099-7924
; Sequence 7924, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7924
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Glycine max
US-11-087-099-7924

Query Match 67.3%; Score 35; DB 11; Length 348;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 8
Db 338 PYVPSC 343

RESULT 12
US-11-188-298-7313
; Sequence 7313, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7313

; LENGTH: 348
; TYPE: PRT
; ORGANISM: Glycine max
US-11-188-298-7313

Query Match 67.3%; Score 35; DB 11; Length 348;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 8
Db 338 PYVPSC 343

RESULT 13
US-11-188-298-16316
; Sequence 16316, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 16316
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Glycine max
US-11-188-298-16316

Query Match 67.3%; Score 35; DB 11; Length 348;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 8
Db 338 PYVPSC 343

RESULT 14
US-11-087-099-12012
; Sequence 12012, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12012
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Glycine max
US-11-087-099-12012

Query Match 67.3%; Score 35; DB 11; Length 358;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PYLPSC 8
Db 340 PYVPSC 345

RESULT 15
US-11-096-568A-3900
; Sequence 3900, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

```

; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3900
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(358)
; OTHER INFORMATION: Ceres Seq. ID no. 13594153
US-11-096-568A-3900

Query Match      67.3%; Score 35; DB 11; Length 358;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 PYLPSC 8
Db      340 PIVPSC 345

Search completed: May 5, 2006, 16:38:48
Job time : 27 secs
```

THIS PAGE BLANK (USPTO)